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OM protein - protein search, using sw model

Run on: September 24, 2004, 14:02:27 ; Search time 51.308 Seconds  
(without alignments)  
659.375 Million cell updates/sec

Title: US-10-661-784-3

Perfect score: 687

Sequence: 1 GSGKDPVQPTTKICVGRD.....VPWEKKIYPTVTVNMECEP 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:.\*  
1: Geneseq1980s:.\*  
2: Geneseq1990s:.\*  
3: Geneseq2000s:.\*  
4: Geneseq2001s:.\*  
5: Geneseq2002s:.\*  
6: Geneseq2003s:.\*  
7: Geneseq2003bs:.\*  
8: Geneseq2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description        |
|------------|-------|-------|--------|-------|--------------------|
| 1          | 618   | 90.0  | 123    | 3     | AA95426 Human hig  |
| 2          | 618   | 90.0  | 304    | 6     | ABP70801 Human ext |
| 3          | 618   | 90.0  | 322    | 6     | ABP70799 Human ext |
| 4          | 618   | 90.0  | 329    | 6     | ABU92044 Human pro |
| 5          | 618   | 90.0  | 358    | 6     | ABP70800 Human ext |
| 6          | 618   | 90.0  | 390    | 6     | ABU99149 Novel hum |
| 7          | 618   | 90.0  | 398    | 6     | ABU99143 Novel hum |
| 8          | 618   | 90.0  | 427    | 8     | ADP76864 Human pro |
| 9          | 618   | 90.0  | 615    | 6     | ABU99144 Novel hum |
| 10         | 618   | 90.0  | 626    | 5     | ABP78707 Human hig |
| 11         | 618   | 90.0  | 644    | 4     | ABG21101 Novel hum |
| 12         | 618   | 90.0  | 644    | 5     | ABP78710 Human hig |
| 13         | 618   | 90.0  | 644    | 6     | ABU99150 Novel hum |
| 14         | 618   | 90.0  | 644    | 6     | ABU99145 Novel hum |
| 15         | 586   | 85.3  | 122    | 3     | ABP7447 Human kin  |
| 16         | 585   | 85.2  | 435    | 4     | ABG21105 Novel hum |
| 17         | 556.5 | 81.0  | 117    | 2     | AAR33350 Domains 3 |
| 18         | 440   | 64.0  | 436    | 1     | AAP40257 Bradykini |
| 19         | 413   | 60.1  | 434    | 1     | AAP40633 Bradykini |
| 20         | 411   | 59.8  | 357    | 6     | ABR41302 Human DIT |
| 21         | 388   | 56.5  | 235    | 5     | ABG60077 Human DIT |
| 22         | 320.5 | 46.7  | 248    | 4     | ABG21102 Novel hum |
| 23         | 316   | 46.0  | 369    | 4     | ABG21099 Novel hum |
| 24         | 190   | 27.7  | 305    | 4     | ABG21100 Novel hum |
| 25         | 171.5 | 25.0  | 167    | 2     | AAW98907 Mouse IMC |

RESULT 1  
AA95426 standard; peptide, 123 AA.

XX AA95426;  
XX AC  
XX XX  
XX DT 25-SEP-2000 (first entry)  
XX DE Human high mol.wt. kininogen domain 3.  
XX XX  
XX KW Anti-angiogenic; angiogenesis; inhibitor; kininogen; homologue; endothelial cell proliferation; apoptosis; cancer; ocular disorder; rheumatoid arthritis; cytostatic; antiarthritic; antirheumatic; therapy; human; D3 peptide.  
XX OS Homo sapiens.  
XX FN WO200035407-A2.  
XX PD 22-JUN-2000.  
XX PF 02-DEC-1999; 99WO-US028465.  
XX PR 16-DEC-1998; 98US-0112427P.  
XX PA (UTEM ) UNIV TEMPLE.  
XX PI (MCCR/) MCCRAE R K.  
XX PI Mcrae RK;  
XX DR WPI; 2000-442247/38.  
XX XX  
XX PT Composition for inhibiting angiogenesis and endothelial cell proliferation, inducing endothelial cell apoptosis and treating cancer, rheumatoid arthritis, and ocular disorders comprises a kininogen domain 3 analog.  
XX PS Disclosure, Page 4; 44pp; English.  
XX XX  
XX CC The present sequence is that of domain 3 of human high mol.wt. kininogen (HK). The invention provides peptides (see AA95405-24) that are analogues of certain sites in the HK domain 3, specifically Asn275-Lys282, Cys426-Cys249, Leu331-Tyr338 and Tyr299-Ser314. The peptides, in which native Cys residues may be replaced by Ala residues, inhibit endothelial cell proliferation and may also induce endothelial cell apoptosis. Compositions including the peptides are used in claimed methods for inhibiting angiogenesis, inhibiting endothelial cell proliferation, and inducing endothelial cell apoptosis. Cancer.

ALIGNMENTS

|    |       |      |     |   |          |
|----|-------|------|-----|---|----------|
| 26 | 166   | 24.2 | 32  | 3 | AA95418  |
| 27 | 163.5 | 23.8 | 126 | 3 | AA95418  |
| 28 | 163.5 | 23.8 | 145 | 2 | AA95418  |
| 29 | 163.5 | 23.8 | 145 | 2 | AA95418  |
| 30 | 163.5 | 23.8 | 145 | 2 | AA95418  |
| 31 | 163.5 | 23.8 | 145 | 2 | AA95418  |
| 32 | 163.5 | 23.8 | 145 | 2 | AA95418  |
| 33 | 163.5 | 23.8 | 145 | 2 | AA95418  |
| 34 | 163.5 | 23.8 | 145 | 2 | AA95418  |
| 35 | 163   | 23.7 | 167 | 7 | ADP14098 |
| 36 | 163   | 23.7 | 167 | 7 | ADP14098 |
| 37 | 161   | 23.4 | 178 | 2 | AA95418  |
| 38 | 157   | 22.9 | 122 | 3 | AA95418  |
| 39 | 154.5 | 22.5 | 127 | 2 | AA95418  |
| 40 | 153   | 22.3 | 127 | 2 | AA95418  |
| 41 | 144.5 | 21.0 | 121 | 3 | AA95418  |
| 42 | 144.5 | 21.0 | 128 | 3 | AA95418  |
| 43 | 143.5 | 20.9 | 121 | 3 | AA95418  |
| 44 | 143.5 | 20.9 | 128 | 3 | AA95418  |
| 45 | 142.5 | 20.7 | 118 | 3 | AA95418  |

CC rheumatoid arthritis, and ocular disorders characterized by undesired  
 CC vascularization of the retina are treated  
 XX  
 SQ Sequence 123 AA;  
 Query Match 90.0%; Score 618; DB 3; Length 123;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-63;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKDVPPTKICVCGPRDIPNTPSPLEBETLTHITIKLNAENATFYFKIDNVKARVQV 62  
 DB 1 GKDVPPTKICVCGPRDIPNTPSPLEBETLTHITIKLNAENATFYFKIDNVKARVQV 60  
 QY 63 AGKYFIDFVARETTCSKESNEELTESCTKLGQSLDCNAEVVVPWEKKIYPTV 118  
 DB 61 AGKYFIDFVARETTCSKESNEELTESCTKLGQSLDCNAEVVVPWEKKIYPTV 116  
 RESULT 2  
 ABP70801  
 ID ABP70801 standard; protein; 304 AA.  
 XX  
 AC ABP70801;  
 XX  
 DT 26-AUG-2003 (first entry)  
 XX  
 DE Human extracellular messenger, EXMES-28.  
 XX  
 KW Human; extracellular messenger; EXMES; cytostatic; antidiabetic;  
 KW immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;  
 KW endocrine disorder; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003018612-A2.  
 XX  
 PD 06-MAR-2003.  
 XX  
 PF 22-AUG-2002; 2002WO-US027213.  
 XX  
 PR 24-AUG-2001; 2001US-0314811P.  
 PR 14-DEC-2001; 2001US-0340584P.  
 PR 18-JAN-2002; 2002US-0350595P.  
 PR 11-MAR-2002; 2002US-0363432P.  
 PR 15-MAR-2002; 2002US-0364607P.  
 PR 05-APR-2002; 2002US-0370761P.  
 PR 24-JUN-2002; 2002US-0391378P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Duggan BM, Lee S, Baughn MR, Hafalia AJA, Wallia NK, Elliott VS,  
 PI Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N;  
 PI Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebardjian Y,  
 PI Richardson TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM;  
 PI Rankumar J;  
 XX  
 DR WPI; 2003-278643/27.  
 DR N-PSDB; ACC42386.  
 XX  
 PT New human extracellular messenger (EXMES) polypeptide, useful for  
 PT preparing a composition for treating a disease associated with decreased  
 PT expression or overexpression of functional EXMES e.g. autoimmune  
 PT disorders or cancer.  
 XX  
 PS Claim 1; Page 207; 22app; English.  
 XX  
 CC The present invention relates to novel human extracellular messenger  
 CC proteins (EXMES-1 to-28; ABP70774-ABP70801) and their coding sequences  
 CC (ACC42361-ACC42386). The proteins are useful for preparing a composition  
 CC for diagnosing or treating a disease or condition associated with  
 CC decreased expression or overexpression of functional EXMES e.g.  
 CC autoimmune/inflammatory disorders, diabetes, endocrine disorders or  
 CC cancer

XX SQ Sequence 304 AA;  
 Query Match 90.0%; Score 618; DB 6; Length 304;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-62;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 GKDVPPTKICVCGPRDIPNTPSPLEBETLTHITIKLNAENATFYFKIDNVKARVQV 62  
 DB 130 GKDVPPTKICVCGPRDIPNTPSPLEBETLTHITIKLNAENATFYFKIDNVKARVQV 189  
 QY 63 AGKYFIDFVARETTCSKESNEELTESCTKLGQSLDCNAEVVVPWEKKIYPTV 118  
 DB 190 AGKYFIDFVARETTCSKESNEELTESCTKLGQSLDCNAEVVVPWEKKIYPTV 245  
 RESULT 3  
 ABP70799  
 ID ABP70799 standard; protein; 322 AA.  
 XX  
 AC ABP70799;  
 XX  
 DT 26-AUG-2003 (first entry)  
 XX  
 DE Human extracellular messenger, EXMES-36.  
 XX  
 KW Human; extracellular messenger; EXMES; cytostatic; antidiabetic;  
 KW immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;  
 KW endocrine disorder; cancer.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003018612-A2.  
 XX  
 PD 06-MAR-2003.  
 XX  
 PF 22-AUG-2002; 2002WO-US027213.  
 XX  
 PR 24-AUG-2001; 2001US-0314811P.  
 PR 14-DEC-2001; 2001US-0340584P.  
 PR 18-JAN-2002; 2002US-0350595P.  
 PR 11-MAR-2002; 2002US-0363432P.  
 PR 15-MAR-2002; 2002US-0364607P.  
 PR 05-APR-2002; 2002US-0370761P.  
 PR 24-JUN-2002; 2002US-0391378P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Duggan BM, Lee S, Baughn MR, Hafalia AJA, Wallia NK, Elliott VS,  
 PI Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N;  
 PI Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebardjian Y,  
 PI Richardson TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM;  
 PI Rankumar J;  
 XX  
 DR WPI; 2003-278643/27.  
 DR N-PSDB; ACC42386.  
 XX  
 PT New human extracellular messenger (EXMES) polypeptide, useful for  
 PT preparing a composition for treating a disease associated with decreased  
 PT expression or overexpression of functional EXMES e.g. autoimmune  
 PT disorders or cancer.  
 XX  
 PS Claim 1; Page 205-206; 22app; English.  
 XX  
 CC The present invention relates to novel human extracellular messenger  
 CC proteins (EXMES-1 to-28; ABP70774-ABP70801) and their coding sequences  
 CC (ACC42361-ACC42386). The proteins are useful for preparing a composition  
 CC for diagnosing or treating a disease or condition associated with  
 CC decreased expression or overexpression of functional EXMES e.g.  
 CC autoimmune/inflammatory disorders, diabetes, endocrine disorders or  
 CC cancer

XX SQ Sequence 322 AA;

Query Match 90.0%; Score 618; DB 6; Length 322;  
 Best Local Similarity 100.0%; Pred. No. 2.1e-62;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GNDVQPTKICVGCPRDIPNTSPLEETLTHITIKLNAENNAFFYFKIDNVKARQVV 62  
 DB 148 GNDVQPTKICVGCPRDIPNTSPLEETLTHITIKLNAENNAFFYFKIDNVKARQVV 207  
 QY 63 AGKVFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVVPWEKKIYPTV 118  
 DB 208 AGKVFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVVPWEKKIYPTV 263

RESULT 4  
 ABU92044  
 ID ABU92044 standard; protein; 329 AA.

XX AC ABU92044;  
 XX DT 15-JUL-2003 (first entry)  
 XX DE Human protein modification and maintenance molecule-24 (PMW-24).  
 XX KW Human; protein modification and maintenance molecule; PMW; cancer;  
 KW cell proliferation disorder; atherosclerosis; neurological disorder;  
 KW epilepsy; Huntington's disease; stroke; immune disorder; allergy;  
 KW inflammatory disorder; AIDS; developmental disorder; hypothyroidism;  
 KW Cushing's syndrome; gastrointestinal disorder; epithelial disorder;  
 KW infection; cytostatic; antiarteriosclerotic; anticonvulsant; nootropic;  
 KW neuroprotective; cerebroprotective; anti-HIV; anti-allergic; vulnary;  
 KW antiinflammatory; thyromimetic.

XX OS Homo sapiens.  
 XX PN WO2003031939-A2.  
 XX PD 17-APR-2003.

XX PP 11-OCT-2002; 2002WO-US032850.

XX PR 12-OCT-2001; 2001US-0329689P.  
 PR 25-OCT-2001; 2001US-0335703P.  
 PR 09-NOV-2001; 2001US-0348887P.  
 PR 28-NOV-2001; 2001US-0334145P.  
 PR 06-DEC-2001; 2001US-0337451P.  
 PR 14-DEC-2001; 2001US-0340584P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Rankumar J, Gorvad AE, Baughn MR, Emerling BM, Yang J, Lee SY;  
 PI Tran UK, Becha SD, Duggan BM, Lee EA, Griffin JA, Li JX;  
 PI Sprague KM, Hafalia AJA, Chawla NK, Lehr-Mason PM, Kable AG, Yue H;  
 PI Marquis JP, Yao MG, Richardson TW, Tang TY, Jin P, Chien D;  
 PI Bhatia U, Burrill JD, Lee S, Blake JJ, Ho A, Zheng W;  
 XX DR WPI, 2003-430274/40.  
 XX DR N-PSDB; ACA92439.

XX PT New human protein modification and maintenance molecules (PMW), useful  
 PT for diagnosing, treating and preventing diseases or conditions associated  
 PT with the aberrant PMW expression e.g. cancer, atherosclerosis, or  
 PT infections.

XX PS Claim 1; Page 264-265; 311pp; English.

XX CC The present invention relates to the isolation of human protein  
 CC modification and maintenance molecules (PMW), and the polynucleotide  
 CC sequences encoding them. A total of 40 PMW polypeptides (designated PMW  
 CC 1 to PMW-40) are disclosed. The sequences of the invention are useful  
 CC for diagnosing a condition or disease associated with the expression of  
 CC PMW in a subject, preparing a polyclonal or monoclonal antibody, and  
 CC generating an expression profile of a sample containing the

CC polynucleotides. The diseases or conditions associated with decreased  
 CC expression or overexpression of PMW are cell proliferation disorders  
 CC (e.g. cancer, atherosclerosis), neurological disorders (e.g. epilepsy,  
 CC Huntington's disease, stroke), immune/inflammatory disorders (e.g. AIDS,  
 CC allergies), developmental disorders (e.g. hypothyroidism, Cushing's  
 CC syndrome), gastrointestinal or epithelial disorders, and infections. The  
 CC PMW polypeptides or their fragments are useful in screening compounds  
 CC for effectiveness as agonists or antagonists of the polypeptides, or in  
 CC altering the expression of the target polynucleotide and compounds that  
 CC specifically bind to, or modulate the activity of the polypeptide.  
 CC ABU92021-ABU92060 represent the human PMW polypeptides of the invention  
 XX  
 XX Sequence 329 AA;

Query Match 90.0%; Score 618; DB 6; Length 329;

Best Local Similarity 100.0%; Pred. No. 2.2e-62;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GNDVQPTKICVGCPRDIPNTSPLEETLTHITIKLNAENNAFFYFKIDNVKARQVV 62  
 DB 155 GNDVQPTKICVGCPRDIPNTSPLEETLTHITIKLNAENNAFFYFKIDNVKARQVV 214  
 QY 63 AGKVFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVVPWEKKIYPTV 118  
 DB 215 AGKVFIDFVARETTCSKESNEELTESCETKLGSLDCNAEVVVPWEKKIYPTV 270

RESULT 5  
 ABP70800

ID ABP70800 standard; protein; 359 AA.

XX AC ABP70800;

XX DT 26-AUG-2003 (first entry)

XX DE Human extracellular messenger, EXMES-27.

XX KW Human; extracellular messenger; EXMES; cytostatic; antidiabetic;  
 KW immunosuppressive; autoimmune disorder; inflammatory disorder; diabetes;  
 KW endocrine disorder; Cancer.

XX OS Homo sapiens.

XX PN WO2003018612-A2.

XX PD 06-MAR-2003.

XX PP 22-AUG-2002; 2002WO-US027213.

XX PR 24-AUG-2001; 2001US-0314811P.  
 PR 14-DEC-2001; 2001US-0340584P.  
 PR 18-JAN-2002; 2002US-0350595P.  
 PR 11-MAR-2002; 2002US-0363432P.  
 PR 15-MAR-2002; 2002US-0364607P.  
 PR 05-APR-2002; 2002US-0370761P.  
 PR 24-JUN-2002; 2002US-0391378P.

XX PA (INCY-) INCYTE GENOMICS INC.

XX PI Duggan BM, Lee S, Baughn MR, Hafalia AJA, Walla NK, Elliott VS;  
 PI Lee SY, Khare R, Wilson AD, Jin P, Hawkins PR, Tang YT, Burford N;  
 PI Ding L, Yao MG, Becha SD, Tran UK, Chien D, Zebajadian Y;  
 PI Richardson TW, Kable AE, Chang H, Swarnakar A, Lehr-Mason PM;  
 PI Rankumar J;

XX DR WPI, 2003-278643/27.

XX DR N-PSDB; ACC42387.

XX PT New human extracellular messenger (EXMES) polypeptide, useful for  
 PT preparing a composition for treating a disease associated with decreased  
 PT expression or overexpression of functional EXMES e.g. autoimmune  
 PT disorders or cancer.

PS Claim 1; Page 206; 224pp; English.

XX The present invention relates to novel human extracellular messenger

CC proteins (EXMES-1 to -28; ABP70774-ABP70801) and their coding sequences

CC (ACC42361-ACC42388). The proteins are useful for preparing a composition

CC for diagnosing or treating a disease or condition associated with

CC decreased expression or overexpression of functional EXMES e.g.

CC autoimmune/inflammatory disorders, diabetes, endocrine disorders or

CC cancer

XX Sequence 358 AA;

SQ

Query Match 90.0%; Score 618; DB 6; Length 358;

Best Local Similarity 100.0%; Pred. No. 2.4e-62;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GKDFVQPPPTKICVGCPRDPTNSPELEETLTHITIKLNAENNAFFPKIDNVKKARVQV 62

DB 184 GKDFVQPPPTKICVGCPRDPTNSPELEETLTHITIKLNAENNAFFPKIDNVKKARVQV 243

OY 63 AGKKYFIDFVARETTCKESNEBELTESCTKKLGSLDCAEYVVPWEKKIYPTV 118

DB 244 AGKKYFIDFVARETTCKESNEBELTESCTKKLGSLDCAEYVVPWEKKIYPTV 299

RESULT 6

ABU99149

ID ABU99149 standard; protein; 390 AA.

AC ABU99149;

XX

XX 01-AUG-2003 (first entry)

XX Novel human GPCR related protein NOV12g.

XX Human; G-protein coupled receptor related protein; GPCR related protein;

KW NOV; cytostatic; cardiac; antiarteriosclerotic; antidiabetic;

KW immunomodulator; anti-HIV; anorectic; antisthmatic; haemostatic;

KW antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine;

KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;

KW diabetes; immune disorder; AIDS; obesity; asthma;

KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease;

KW infection; multiple sclerosis; cancer-associated cachexia;

KW wasting disorder; chronic disease; neurogenesis; cell differentiation;

KW cell proliferation; haematopoiesis; wound healing; angiogenesis;

KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.

XX Homo sapiens.

XX

XX WO2002299116-A2.

XX

XX 12-DEC-2002.

XX

XX 04-JUN-2002; 2002WO-US017428.

XX

XX 04-JUN-2001; 2001US-0295607P.

PR 04-JUN-2001; 2001US-0295661P.

PR 06-JUN-2001; 2001US-0296404P.

PR 06-JUN-2001; 2001US-0296418P.

PR 14-JUN-2001; 2001US-0298285P.

PR 15-JUN-2001; 2001US-0298554P.

PR 21-JUN-2001; 2001US-0299949P.

PR 26-JUN-2001; 2001US-0300881P.

PR 28-JUN-2001; 2001US-0301509P.

PR 13-AUG-2001; 2001US-0311972P.

PR 29-AUG-2001; 2001US-0315071P.

PR 14-SEP-2001; 2001US-0322291P.

PR 17-SEP-2001; 2001US-0322706P.

PR 14-DEC-2001; 2001US-0341186P.

PR 28-FEB-2002; 2002US-0361189P.

PR 12-MAR-2002; 2002US-0363673P.

PR 12-MAR-2002; 2002US-0363676P.

PR 03-JUN-2002; 2002US-00363676.

PA (CURA-) CURAGEN CORP.

XX Anderson DW, Baugattner JC, Boldog PL, Casman SJ, Edinger SR;

XX Maggioni EA, Gerlach VL, Gorman L, Guo X, Hjalt T, Kekuda R, Li L;

PI MacDougall JR, Malyankar UM, Millet I, Padigaru M, Patturajan M;

PI Pena CE, Rastelli L, Shinkens RA, Stone DJ, Spytek RA, Vernet CM;

PI Voss EZ, Zerhusen BD;

XX WPI; 2003-140627/13.

DR N-PSDB; ACD03653.

XX New NOVX polypeptides and nucleic acids, useful for preventing or

PT treating NOVX-associated disorders e.g. cancer, cardiomyopathy,

PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or

PT pharmacogenomics.

XX

PS Claim 1; Page 147; 332pp; English.

XX The invention describes an isolated polypeptide (1) comprising any of 27

CC 118-961 residue amino acid sequences, given in the specification, a

CC mature form of them, a sequence that is at least 95 % identical to them,

CC or a sequence having one or more conservative substitutions in them. The

CC polypeptide is useful in manufacturing a medicament for treating a

CC syndrome associated with a human disease selected from a pathology

CC associated with the polypeptide. The NOVX polypeptides, polynucleotides

CC and antibodies are useful in treating or preventing NOVX-associated

CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune

CC diseases, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's

CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-

CC associated cachexia, and other wasting disorders associated with chronic

CC diseases. The nucleic acids and polypeptides may also be used as targets

CC for the identification of small molecules that modulate or inhibit e.g.

CC neurogenesis, cell differentiation, cell proliferation, haematopoiesis,

CC wound healing and angiogenesis, in gene therapy, in generation of

CC antibodies that bind immunospecifically to NOVX substances for use in

CC therapeutic or diagnostic methods. The nucleic acids are further used as

CC hybridization probes, in chromosome mapping, tissue typing, preventive

CC medicine, and pharmacogenomics. The polypeptides are also useful as

CC vaccines. This is the amino acid sequence of a novel human G-protein

CC coupled receptor related protein NOV

XX Sequence 390 AA;

SQ

Query Match 90.0%; Score 618; DB 6; Length 390;

Best Local Similarity 100.0%; Pred. No. 2.7e-62;

Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GKDFVQPPPTKICVGCPRDPTNSPELEETLTHITIKLNAENNAFFPKIDNVKKARVQV 62

DB 216 GKDFVQPPPTKICVGCPRDPTNSPELEETLTHITIKLNAENNAFFPKIDNVKKARVQV 275

OY 63 AGKKYFIDFVARETTCKESNEBELTESCTKKLGSLDCAEYVVPWEKKIYPTV 118

DB 276 AGKKYFIDFVARETTCKESNEBELTESCTKKLGSLDCAEYVVPWEKKIYPTV 331

RESULT 7

ABU99143

ID ABU99143 standard; protein; 398 AA.

AC ABU99143;

XX

XX 01-AUG-2003 (first entry)

XX Novel human GPCR related protein NOV12a.

XX Human; G-protein coupled receptor related protein; GPCR related protein;

KW NOV; cytostatic; cardiac; antiarteriosclerotic; antidiabetic;

KW immunomodulator; anti-HIV; anorectic; antisthmatic; haemostatic;

KW antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine;

KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;

KW diabetes; immune disorder; AIDS; obesity; asthma;  
 KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease;  
 KW infection; multiple sclerosis; cancer-associated cachexia;  
 KW wasting disorder; chronic disease; neurogenesis; cell differentiation;  
 KW cell proliferation; haematopoiesis; wound healing; angiogenesis;  
 KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.  
 OS Homo sapiens.

XX WO200299116-A2.

XX PD 12-DEC-2002.

XX PF 04-JUN-2002; 2002WO-US017428.

XX PR 04-JUN-2001; 2001US-0295607P.

XX PR 06-JUN-2001; 2001US-0295661P.

XX PR 06-JUN-2001; 2001US-0296404P.

XX PR 06-JUN-2001; 2001US-0296418P.

XX PR 14-JUN-2001; 2001US-0298285P.

XX PR 15-JUN-2001; 2001US-0298556P.

XX PR 21-JUN-2001; 2001US-0299949P.

XX PR 26-JUN-2001; 2001US-0300883P.

XX PR 28-JUN-2001; 2001US-0301550P.

XX PR 13-AUG-2001; 2001US-0311972P.

XX PR 27-AUG-2001; 2001US-0315071P.

XX PR 29-AUG-2001; 2001US-0315660P.

XX PR 14-SEP-2001; 2001US-0322293P.

XX PR 17-SEP-2001; 2001US-032708P.

XX PR 14-DEC-2001; 2001US-0341186P.

XX PR 28-FEB-2002; 2002US-0361189P.

XX PR 12-MAR-2002; 2002US-0363673P.

XX PR 13-MAR-2002; 2002US-0363676P.

XX PR 03-JUN-2002; 2002US-00363676.

XX PA (CURA-) CURAGEN CORP.

XX PI Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR,  
 PI Gargoli EA, Gerlach VL, Gorman L, Guo X, Hjalte T, Kekuda R, Li L,  
 PI Macdougall JR, Malyankar UM, Millet I, Padigaru M, Parturajan M,  
 PI Pena CE, Rastelli L, Shinkens RA, Stone DJ, Spytek XA, Varnet CM,  
 PI Voss EZ, Zornhusen BD;  
 XX WPI; 2003-140627/13.  
 DR N-PSDB; ACD03647.

XX PT New NOVX polypeptides and nucleic acids, useful for preventing or  
 PT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
 PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
 PT pharmacogenomics.

XX PS Claim 1; Page 143; 332pp; English.

XX CC The invention describes an isolated polypeptide (I) comprising any of 27  
 CC 118-961 residue amino acid sequences, given in the specification, a  
 CC mature form of them, a sequence that is at least 95 % identical to them,  
 CC or a sequence having one or more conservative substitutions in them. The  
 CC polypeptide is useful in manufacturing a medicament for treating a  
 CC syndrome associated with a human disease selected from a pathology  
 CC associated with the polypeptide. The NOVX polypeptides, polynucleotides  
 CC and antibodies are useful in treating or preventing NOVX-associated  
 CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune  
 CC disorders, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's  
 CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-  
 CC associated cachexia, and other wasting disorders associated with chronic  
 CC diseases. The nucleic acids and polypeptides may also be used as targets  
 CC for the identification of small molecules that modulate or inhibit e.g.  
 CC neurogenesis, cell differentiation, cell proliferation, haematopoiesis,  
 CC wound healing and angiogenesis, in gene therapy, in generation of  
 CC antibodies that bind immunospecifically to NOVX substances for use in  
 CC therapeutic or diagnostic methods. The nucleic acids are further used as  
 CC hybridisation probes, in chromosome mapping, tissue typing, preventive  
 CC medicine, and pharmacogenomics. The polypeptides are also useful as

CC vaccines. This is the amino acid sequence of a novel human G-protein  
 CC coupled receptor related protein NOV

XX Sequence 398 AA;

XX Query Match 90.0%; Score 618; DB 6; Length 398;

XX Best Local Similarity 100.0%; Pred. No. 2.8e-62; Indels 0; Gaps 0;

XX Matches 116; Conservative 0; Mismatches 0;

XX QY 3 GKDFVQPTKICVGCPRDIPNTSPELETLTHITIKLAENNAFTYFKINDVKKARQVV 62

XX DB 224 GKDFVQPTKICVGCPRDIPNTSPELETLTHITIKLAENNAFTYFKINDVKKARQVV 283

XX QY 63 AGKKYFDVFVARETTCKSNBELTESCTKGLGSLDCNAEVVVPWEKKIYPTV 118

XX DB 284 AGKKYFDVFVARETTCKSNBELTESCTKGLGSLDCNAEVVVPWEKKIYPTV 339

XX RESULT 8

XX ADE76864

XX ID ADE76864 standard; protein; 427 AA.

XX AC ADE76864;

XX DT 29-JAN-2004 (first entry)

XX DE Human protein expressed in a liver disorder #9.

XX KW human; liver disorder; hyperlipidaemia; hypertension; type II diabetes;

XX KW tumour; liver; inflammatory disorder; immune response disorder;

XX KW high-throughput screening; differential gene expression; gene therapy.

XX OS Homo sapiens.

XX FN US2003108871-A1.

XX PD 12-JUN-2003.

XX PF 30-JUL-2001; 2001US-00919039.

XX PR 28-JUL-2000; 2000US-0222113P.

XX PA (KASE/) KASER M R.

XX PI Kaser MR;

XX DR WPI; 2004-031227/03.

XX DR N-PSDB; ADE76863.

XX PT Composition comprising several cDNAs that are differentially expressed in  
 PT treated human C3A liver cell cultures, useful for treating liver  
 PT disorders.

XX PS Claim 1; SEQ ID NO 29; 41pp; English.

XX CC The invention relates to a composition comprising several cDNAs that are  
 CC differentially expressed in a liver disorder. The composition is useful  
 CC for treating liver disorder such as hyperlipidaemia, hypertension, type  
 CC II diabetes, tumours of the liver and disorders of the inflammatory and  
 CC immune response. The composition is useful for a high-throughput method  
 CC of screening several molecules or compounds to identify a ligand which  
 CC specifically binds a cDNA. A protein encoded by the cDNA is useful for a  
 CC high-throughput method for using a protein to screen several molecules or  
 CC compounds to identify at least one ligand which specifically binds the  
 CC protein which involves combining the protein encoded by the cDNA with  
 CC several of molecules or compounds under conditions to allow specific  
 CC binding, and detecting specific binding between the protein and a  
 CC molecule or compound, therefore identifying a ligand which specifically  
 CC binds the protein. The composition is useful for detecting and  
 CC quantifying differential gene expression, can be used in gene therapy, to  
 CC formulate prognosis and to design a treatment regimen and to monitor the  
 CC efficacy of treatment. The present sequence represents the amino acid  
 CC sequence of a protein encoded by a cDNA differentially expressed in a

CC liver disorder.  
XX Sequence 427 AA;  
SQ

Query Match 90.0%; Score 618; DB 8; Length 427;  
Best Local Similarity 100.0%; Pred. No. 3.1e-62;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPQPTKICVCGPRDIPNTSPLEETLTITIKLNAENNTFFPKIDNVKARVQV 62  
DB 253 GKDVPQPTKICVCGPRDIPNTSPLEETLTITIKLNAENNTFFPKIDNVKARVQV 312

QY 63 AGKXYFIDFVARETTCKESNEELTSCETKLGQSLDCNAEVVVPWEKKIYPTV 118  
DB 313 AGKXYFIDFVARETTCKESNEELTSCETKLGQSLDCNAEVVVPWEKKIYPTV 368

RESULT 9  
ID ABU99144 standard; protein: 615 AA.  
AC ABU99144;  
XX  
XX  
XX 01-AUG-2003 (first entry)  
XX  
XX Novel human GPCR related protein NOV12b.  
XX  
XX Human; G-protein coupled receptor related protein; GPCR related protein;  
XX NOV; cytosolic; cardiac; antiarrhythmic; anti-diabetic;  
XX immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic;  
XX antiparkinsonian; neuroprotective; nontropic; gene therapy; vaccine;  
XX NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;  
XX diabetes; immune disorder; AIDS; obesity; asthma;  
XX haematopoietic disorder; Parkinson's disease; Alzheimer's disease;  
XX wasting disorder; chronic scleroderma; cancer-associated cachexia;  
XX cell proliferation; haematopoiesis; wound healing; angiogenesis;  
XX chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.  
XX  
XX Homo sapiens.  
XX  
XX WO200299116-A2.  
XX  
XX 12-DEC-2002.  
XX  
XX 04-JUN-2002; 2002WO-US017428.  
XX  
XX 04-JUN-2001; 2001US-0295607P.  
XX 04-JUN-2001; 2001US-0295661P.  
XX 06-JUN-2001; 2001US-0296404P.  
XX 06-JUN-2001; 2001US-0296418P.  
XX 14-JUN-2001; 2001US-0298285P.  
XX 15-JUN-2001; 2001US-0298556P.  
XX 21-JUN-2001; 2001US-0299949P.  
XX 26-JUN-2001; 2001US-0300838P.  
XX 28-JUN-2001; 2001US-0301550P.  
XX 13-AUG-2001; 2001US-0311972P.  
XX 27-AUG-2001; 2001US-0315071P.  
XX 29-AUG-2001; 2001US-0315660P.  
XX 14-SEP-2001; 2001US-0322293P.  
XX 17-SEP-2001; 2001US-0322706P.  
XX 18-DEC-2001; 2001US-0341186P.  
XX 28-FEB-2002; 2002US-0361189P.  
XX 12-MAR-2002; 2002US-0363673P.  
XX 12-MAR-2002; 2002US-0363676P.  
XX 03-JUN-2002; 2002US-00363676.  
XX  
XX (CURA-) CURAGEN CORP.  
XX  
XX Anderson DW, Baumgartner JC, Boldog FB, Casman SJ, Edinger SR;  
XX Gangoli EA, Gerlach VL, Gorman L, Guo X, Hjalte T, Kekuda R, Li L;  
XX MacDougall JR, Malyankar DN, Millet I, Padigaru M, Patturajan M;  
XX Pena CEA, Rastelli L, Shimkete RA, Stone DJ, Szytko KA, Vernet CAM;

PI Voss EZ; Zerhusen BD;  
XX WPI; 2003-140627/13.  
XX N-ESDS; AC03648.  
XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
XX treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,  
XX atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
XX pharmacogenomics.  
XX  
XX Claim 1; Page 144; 332pp; English.  
XX  
XX The invention describes an isolated polypeptide (1) comprising any of 27  
XX 118-961 residue amino acid sequences, given in the specification, a  
XX mature form of them, a sequence that is at least 95 % identical to them,  
XX or a sequence having one or more conservative substitutions in them. The  
XX polypeptide is useful in manufacturing a medicament for treating a  
XX syndrome associated with a human disease selected from a pathology  
XX associated with the polypeptide. The NOVX polypeptides, polynucleotides  
XX and antibodies are useful in treating or preventing NOVX-associated  
XX disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune  
XX disease, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's  
XX disease, Alzheimer's disease, infectious multiple sclerosis, cancer-  
XX associated cachexia, and other wasting disorders associated with chronic  
XX diseases. The nucleic acids and polypeptides may also be used as targets  
XX for the identification of small molecules that modulate or inhibit e.g.  
XX neurogenesis, cell differentiation, cell proliferation, haematopoiesis,  
XX wound healing and angiogenesis, in gene therapy, in generation of  
XX antibodies that bind immunospecifically to NOVX substances for use in  
XX therapeutic or diagnostic methods. The nucleic acids are further used as  
XX hybridization probes, in chromosome mapping, tissue typing, preventive  
XX medicine, and pharmacogenomics. The polypeptides are also useful as  
XX vaccines. This is the amino acid sequence of a novel human G-protein  
XX coupled receptor related protein NOV  
XX  
XX Sequence 615 AA;  
SQ

Query Match 90.0%; Score 618; DB 6; Length 615;  
Best Local Similarity 100.0%; Pred. No. 5.1e-62;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDVPQPTKICVCGPRDIPNTSPLEETLTITIKLNAENNTFFPKIDNVKARVQV 62  
DB 224 GKDVPQPTKICVCGPRDIPNTSPLEETLTITIKLNAENNTFFPKIDNVKARVQV 283

QY 63 AGKXYFIDFVARETTCKESNEELTSCETKLGQSLDCNAEVVVPWEKKIYPTV 118  
DB 284 AGKXYFIDFVARETTCKESNEELTSCETKLGQSLDCNAEVVVPWEKKIYPTV 339

RESULT 10  
ID AB78707  
XX  
XX AB78707 standard; protein: 626 AA.  
XX  
XX AB78707;  
XX  
XX 18-JUL-2002 (first entry)  
XX  
XX Human high molecular weight kininogen (HK) mature protein SEQ ID NO:1.  
XX  
XX Human; kininogen; high molecular weight kininogen; HK; D5 domain;  
XX D5 receptor; angiogenesis; endothelial cell; cytotactic; antitumour;  
XX antiatherosclerotic; vasotropic; vulnary; tranquilliser; thrombolytic;  
XX ophthalmological; gynaecological; antitumor; antidiabetic; antiarthritic;  
XX antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.  
XX  
XX Homo sapiens.  
XX  
XX  
XX Key Location/Qualifiers  
XX Domain 384..508  
XX /label= D5\_domain  
XX  
XX WO200214369-A2.

XX PD 21-FEB-2002.  
 XX XX  
 XX PF 24-JUL-2001; 2001WO-US033185.  
 XX XX  
 XX PR 24-JUL-2000; 2000US-0220194P.  
 XX XX  
 XX PA (ATTE-) ATTENUON LLC.  
 XX XX  
 XX PI Mazar AP, Juarez JC;  
 XX XX  
 XX DR WPI; 2002-393611/42.  
 XX XX  
 XX PT Novel human kininogen D5 domain polypeptides useful for treating  
 XX PT conditions associated with endothelial cell migration, proliferation,  
 XX PT invasion or angiogenesis, e.g. arthritis, macular degeneration, benign  
 XX PT hyperplasia.  
 XX PS  
 XX PS Disclosure; Page 13; 84pp; English.  
 XX CC The present invention describes an isolated polypeptide (I) that  
 CC corresponds to the D5 domain of human kininogen, or biologically active  
 CC peptide fragment, homologue or functional derivative, and which: (a)  
 CC inhibits angiogenesis; (b) binds to the D5 binding site on endothelial  
 CC cells (EC); (c) activates signalling pathways leading to the introduction  
 CC of apoptosis in EC; and/or (d) inhibits the signalling pathway required  
 CC for maintenance of EC viability. (I) has cytostatic, antitumour,  
 CC antiatherosclerotic, vasotropic, antiulcer, tranquiliser, thrombolytic,  
 CC ophthalmological, gynaecological, antiulcer, antidiabetic, antiarthritic,  
 CC antiangiogenic, antiapoptotic and endocrine activities. An antibody (IX)  
 CC specific for an epitope of (I) is useful for inhibiting tumour growth or  
 CC angiogenesis in a subject. (I), a D5 fusion polypeptide (II) or a dimeric  
 CC or trimeric fusion polypeptide (III) can be used for inhibiting EC  
 CC migration, proliferation, invasion, or angiogenesis, or for inducing EC  
 CC apoptosis. An angiogenic EC-targeting pharmaceutical composition (X)  
 CC comprising (I), (II), or (III), can be used for treating a subject having  
 CC a disease or condition associated with undesired EC migration,  
 CC proliferation, invasion or angiogenesis. (I), (II), or (III) can be used  
 CC for isolating a D5 domain binding molecule from a complex mixture and for  
 CC isolating or enriching cells expressing D5 domain binding sites from a  
 CC cell mixture. The present sequence represents the mature human high  
 CC molecular weight kininogen (HK) protein, which is given in the  
 CC exemplification of the present invention  
 XX SQ Sequence 626 AA;  
 Query Match 90.0%; Score 618; DB 5; Length 626;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-62;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 GKDVPPTKICVCGPRDPTNSPELETLTHITKLNANNATFYFKIDNVKARQVQV 62  
 Db 235 GKDVPPTKICVCGPRDPTNSPELETLTHITKLNANNATFYFKIDNVKARQVQV 294  
 Qy 63 AGKXYFIDFVARETTCSKESNEELTESCTKGLQSLDCNAEYVVPWEKKIYPTV 118  
 Db 295 AGKXYFIDFVARETTCSKESNEELTESCTKGLQSLDCNAEYVVPWEKKIYPTV 350  
 RESULT 11  
 ID ABG21101 standard; protein; 644 AA.  
 AC ABG21101;  
 XX ABG21101;  
 XX 18-FEB-2002 (first entry)  
 XX Novel human diagnostic protein #21092.  
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX Homo sapiens.  
 OS

XX WO200175067-A2.  
 XX PD 11-OCT-2001.  
 XX XX  
 XX XX 30-MAR-2001; 2001WO-US008631.  
 XX XX  
 XX XX 31-MAR-2000; 2000US-00540217.  
 XX PR 23-AUG-2000; 2000US-00649167.  
 XX XX  
 XX XX (HYSE-) HYSEQ INC.  
 XX XX  
 XX PI Dmanac RT, Liu C, Tang YT;  
 XX XX  
 XX XX WPI; 2001-639162/73.  
 XX DR N-PSDB; AS88288.  
 XX XX  
 XX PT New isolated polynucleotide and encoded polypeptides, useful in  
 XX PT diagnostics, forensics, gene mapping, identification of mutations  
 XX PT responsible for genetic disorders or other traits and to assess  
 XX PT biodiversity.  
 XX PS  
 XX PS Claim 20; SEQ ID NO 51460; 103pp; English.  
 XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activities. The  
 CC polypeptide and polynucleotide sequences have application in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG0377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 644 AA;  
 Query Match 90.0%; Score 618; DB 4; Length 644;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-62;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 GKDVPPTKICVCGPRDPTNSPELETLTHITKLNANNATFYFKIDNVKARQVQV 62  
 Db 253 GKDVPPTKICVCGPRDPTNSPELETLTHITKLNANNATFYFKIDNVKARQVQV 312  
 Qy 63 AGKXYFIDFVARETTCSKESNEELTESCTKGLQSLDCNAEYVVPWEKKIYPTV 118  
 Db 313 AGKXYFIDFVARETTCSKESNEELTESCTKGLQSLDCNAEYVVPWEKKIYPTV 368  
 RESULT 12  
 ID ABB78710  
 XX ABB78710 standard; protein; 644 AA.  
 AC ABB78710;  
 XX ABB78710;  
 XX 18-JUL-2002 (first entry)  
 XX Human high molecular weight kininogen (HK) protein.  
 DE Human; kininogen; high molecular weight kininogen; HK; D5 domain;  
 KW D5 receptor; angiogenesis; endothelial cell; cytostatic; antitumour;  
 KW



KW antiatherosclerotic; vasotropic; vulnerary; tranquilliser; thrombolytic;  
 KW ophthalmological; gynaecological; antiulcer; antidiabetic; antiarthritic;  
 KW antiangiogenic; antiapoptotic; endocrine; apoptosis; gene therapy.  
 XX Homo sapiens.

| Key            | Location/Qualifiers                                |
|----------------|--|
| Peptide        | 1..18  |
| Protein        | /label= signal                                     |
|                | 19..644  |
|                | /label= mature_human_high_molecular_weight_kinogen |
| Disulfide-bond | 28..614  |
| Disulfide-bond | 83..94   |
| Disulfide-bond | 107..126   |
| Disulfide-bond | 142..145   |
| Disulfide-bond | 206..218   |
| Disulfide-bond | 229..248   |
| Disulfide-bond | 264..267   |
| Disulfide-bond | 328..340   |
| Disulfide-bond | 351..370   |
| Domain         | 402..526   |
|                | /label= D5_domain                                  |

WO200214369-A2.

21-FEB-2002.

24-JUL-2001; 2001WO-US023185.

24-JUL-2000; 2000US-0220194P.

(ATTE-) ATTENUON LLC.

Mazar AP, Juarez JC;

WPI; 2002-393611/42.

Novel human kinogen D5 domain polypeptides useful for treating conditions associated with endothelial cell migration, proliferation, invasion or angiogenesis, e.g. arthritis, macular degeneration, benign hyperplasia.

Disclosure: Fig 1B-E; 84pp; English.

The present invention describes an isolated polypeptide (I) that corresponds to the D5 domain of human kinogen, or biologically active peptide fragment, homologue or functional derivative, and which: (a) inhibits angiogenesis; (b) binds to the D5 binding site on endothelial cells (EC); (c) activates signalling pathways leading to the introduction of apoptosis in EC; and/or (d) inhibits the signalling pathway required for maintenance of EC viability. (I) has cytostatic, antitumour, antiatherosclerotic, vasotropic, vulnerary, tranquilliser, thrombolytic, ophthalmological, gynaecological, antiulcer, antidiabetic, antiarthritic, antiangiogenic, antiapoptotic and endocrine activities. An antibody (IX) specific for an epitope of (I) is useful for inhibiting tumour growth or angiogenesis in a subject. (II), a D5 fusion polypeptide (II) or a dimeric or trimeric fusion polypeptide (III) can be used for inhibiting EC migration, proliferation, invasion, or angiogenesis, or for inducing EC apoptosis. An angiogenic EC-targeting pharmaceutical composition (X) comprising (I), (II), or (III), can be used for treating a subject having a disease or condition associated with undesired EC migration, proliferation, invasion or angiogenesis. (I), (II), or (III) can be used for isolating a D5 domain binding molecule from a complex mixture and for isolating or enriching cells expressing D5 domain binding sites from a cell mixture. The present sequence represents the human high molecular weight kinogen (HK) protein, which is given in the exemplification of the present invention.

Sequence 644 AA;

Query Match 90.0%; Score 618; DB 5; Length 644;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-62;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| QY | 3   | QKDFVQPTKICVCPDIDPTNSPELBEFLTHTITKLAENNTATFYKIDNVKARQVV 62  |
|----|-----|---|
| DB | 253 | GKDFVQPTKICVCPDIDPTNSPELBEFLTHTITKLAENNTATFYKIDNVKARQVV 312 |
| QY | 63  | AGKYPIDFVARETTCSKESNEELTSCETKXKLGSLDCNARFVYVVPWEKKIYPTV 118 |
| DB | 313 | AGKYPIDFVARETTCSKESNEELTSCETKXKLGSLDCNARFVYVVPWEKKIYPTV 368 |

# RESULT 13

ASU99150  
 ID ASU99150 standard; protein; 644 AA.

XX AC ASU99150;

XX DI 01-AUG-2003 (first entry)

DE DE Novel human GPCR related protein NOV12h.

KW Human; G-protein coupled receptor related protein; GPCR related protein;  
 KW NOV; cytostatic; cardiant; antiarteriosclerotic; antidiabetic;  
 KW immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic;  
 KW antiparkinsonian; neuroprotective; nootropic; gene therapy; vaccine;  
 KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;  
 KW diabetes; immune disorder; AIDS; obesity; asthma;  
 KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease;  
 KW infection; multiple sclerosis; cancer-associated cachexia;  
 KW wasting disorder; chronic disease; neurogenesis; cell differentiation;  
 KW cell proliferation; haematopoiesis; wound healing; angiogenesis;  
 KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.

XX OS Homo sapiens.

XX FN WO2002299116-A2.

XX PD 12-DEC-2002.

XX PF 04-JUN-2002; 2002WO-US017428.

XX PR 04-JUN-2001; 2001US-0295607P.

XX PR 04-JUN-2001; 2001US-0235661P.

XX PR 06-JUN-2001; 2001US-0256404P.

XX PR 06-JUN-2001; 2001US-0256418P.

XX PR 14-JUN-2001; 2001US-0298285P.

XX PR 15-JUN-2001; 2001US-0298556P.

XX PR 21-JUN-2001; 2001US-0299949P.

XX PR 26-JUN-2001; 2001US-0300883P.

XX PR 13-AUG-2001; 2001US-0311972P.

XX PR 27-AUG-2001; 2001US-0315071P.

XX PR 29-AUG-2001; 2001US-0315660P.

XX PR 14-SEP-2001; 2001US-0322293P.

XX PR 17-SEP-2001; 2001US-0322706P.

XX PR 14-DEC-2001; 2001US-0341186P.

XX PR 28-FEB-2002; 2002US-0361189P.

XX PR 12-MAR-2002; 2002US-0363673P.

XX PR 03-JUN-2002; 2002US-00363676.

(CURA-) CURAGEN CORP.

XX PA Anderson DW, Baumgartner JC, Boldog FL, Casman SJ, Edinger SR;  
 XX PI Gargolli EA, Gerlach VL, Gorman L, Guo X, Hjalte T, Kekuda R, Li L;  
 XX PI MacDougall JR, Malyankar UM, Millet I, Padigaru M, Patturajan M;  
 XX PI Pena CEA, Restelli L, Shinketa RA, Stone DJ, Spytek KA, Vernet CM;  
 XX PI Voss EZ, Zerhusen BD;  
 XX DR WPI; 2003-140627/13.  
 XX DR N-PSDB; AC003654.  
 XX FT New NOVX polypeptides and nucleic acids, useful for preventing or  
 XX FT treating NOVX-associated disorders, e.g. cancer, cardiomyopathy,



PT atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
pharmacogenomics.  
XX Claim 1, Page 148; 332pp; English.  
XX  
CC The invention describes an isolated polypeptide (I) comprising any of 27  
CC 118-961 residue amino acid sequences, given in the specification, a  
CC mature form of them, a sequence that is at least 95 % identical to them,  
CC or a sequence having one or more conservative substitutions in them. The  
CC polypeptide is useful in manufacturing a medicament for treating a  
CC syndrome associated with a human disease selected from a pathology  
CC associated with the polypeptide. The NOVX polypeptides, polynucleotides  
CC and antibodies are useful in treating or preventing NOVX-associated  
CC disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune  
CC disorders, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's  
CC disease, Alzheimer's disease, infections, multiple sclerosis, cancer-  
CC associated cachexia, and other wasting disorders associated with chronic  
CC diseases. The nucleic acids and polypeptides may also be used as targets  
CC for the identification of small molecules that modulate or inhibit e.g.  
CC neurogenesis, cell differentiation, cell proliferation, haematopoiesis,  
CC wound healing and angiogenesis, in gene therapy, in generation of  
CC antibodies that bind immunospecifically to NOVX substances for use in  
CC therapeutic or diagnostic methods. The nucleic acids are further used as  
CC hybridisation probes, in chromosome mapping, tissue typing, preventive  
CC medicine, and pharmacogenomics. The polypeptides are also useful as  
CC vaccines. This is the amino acid sequence of a novel human G-protein  
CC coupled receptor related protein NOV  
XX  
SQ Sequence 644 AA;  
Query Match 90.0%; Score 618; DB 6; Length 644;  
Best Local Similarity 100.0%; Pred. No. 5.5e-62;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GKDFVQPTKICVCGPRDIPNPSPELEETLTHITKLNAENNAIFYKIDNVKARQV 62  
DB 253 GKDFVQPTKICVCGPRDIPNPSPELEETLTHITKLNAENNAIFYKIDNVKARQV 312  
QY 63 AGKYTFIDFVARETTCSKESNEELTESCETKKGQSLDCNAEYVVPPEKKIYPTV 118  
DB 313 AGKYTFIDFVARETTCSKESNEELTESCETKKGQSLDCNAEYVVPPEKKIYPTV 368  
RESULT 14  
ABU99145  
ID ABU99145 standard; protein; 644 AA.  
AC ABU99145;  
XX  
XX 01-AUG-2003 (first entry)  
DE Novel human GPCR related protein NOV12c.  
XX Human; G-protein coupled receptor related protein; GPCR related protein;  
KW NOV; cytosolic; cardiac; antiarteriosclerotic; antidiabetic;  
KW immunomodulator; anti-HIV; anorectic; antiasthmatic; haemostatic;  
KW anti-parkinsonian; neuroprotective; nootropic; gene therapy; vaccine;  
KW NOVX-associated disorder; cardiomyopathy; atherosclerosis; cancer;  
KW diabetes; immune disorder; AIDS; obesity; asthma;  
KW haematopoietic disorder; Parkinson's disease; Alzheimer's disease;  
KW infection; multiple sclerosis; cancer-associated cachexia;  
KW wasting disorder; chronic disease; neurogenesis; cell differentiation;  
KW cell proliferation; haematopoiesis; wound healing; angiogenesis;  
KW chromosome mapping; tissue typing; preventive medicine; pharmacogenomic.  
XX Homo sapiens.  
OS  
XX WO200299116-A2.  
PN  
XX  
XX 12-DEC-2002.  
PD  
XX  
XX 04-JUN-2002; 2002WO-US017428.  
PP  
XX

PR 04-JUN-2001; 2001US-0295607P.  
PR 04-JUN-2001; 2001US-0295661P.  
PR 06-JUN-2001; 2001US-0296404P.  
PR 06-JUN-2001; 2001US-0296418P.  
PR 14-JUN-2001; 2001US-0298285P.  
PR 18-JUN-2001; 2001US-0298556P.  
PR 21-JUN-2001; 2001US-0299949P.  
PR 28-JUN-2001; 2001US-0300883P.  
PR 28-JUN-2001; 2001US-0301550P.  
PR 13-AUG-2001; 2001US-0311972P.  
PR 27-AUG-2001; 2001US-0315071P.  
PR 29-AUG-2001; 2001US-0315660P.  
PR 14-SEP-2001; 2001US-032293P.  
PR 17-SEP-2001; 2001US-0322706P.  
PR 14-DEC-2001; 2001US-0341186P.  
PR 28-FEB-2002; 2002US-0361189P.  
PR 12-MAR-2002; 2002US-0361673P.  
PR 12-MAR-2002; 2002US-0361676P.  
PR 03-JUN-2002; 2002US-00363676.  
XX (CURA-) CUPAGEN CORP.  
PA  
XX Anderson DW, Baumgartner JC, Boldog PL, Casman SJ, Edinger SR,  
XX Gangoli EA, Gerlach VL, Gorman L, Guo X, Hjalit T, Kekuda R, Li L,  
XX McDougall JR, Malyankar UM, Millet I, Padigaru M, Patturajan M,  
XX Pena CE, Rastelli L, Shinkets RA, Stone DJ, Spytek KA, Vernet CAM,  
XX Voss EZ, Zerhusen BD,  
XX WPI; 2003-140627/13.  
DR N-PSDB; ACD03649.  
XX  
XX New NOVX polypeptides and nucleic acids, useful for preventing or  
XX treating NOVX-associated disorders, e.g. cancer, cardiomyopathy, or  
XX atherosclerosis, or diabetes, and in chromosome mapping, tissue typing or  
XX pharmacogenomics.  
XX  
XX Claim 1, Page 144-145; 332pp; English.  
XX  
XX The invention describes an isolated polypeptide (I) comprising any of 27  
XX 118-961 residue amino acid sequences, given in the specification, a  
XX mature form of them, a sequence that is at least 95 % identical to them,  
XX or a sequence having one or more conservative substitutions in them. The  
XX polypeptide is useful in manufacturing a medicament for treating a  
XX syndrome associated with a human disease selected from a pathology  
XX associated with the polypeptide. The NOVX polypeptides, polynucleotides  
XX and antibodies are useful in treating or preventing NOVX-associated  
XX disorders, e.g. cardiomyopathy, atherosclerosis, cancer, diabetes, immune  
XX disorders, AIDS, obesity, asthma, haematopoietic disorders, Parkinson's  
XX disease, Alzheimer's disease, infections, multiple sclerosis, cancer-  
XX associated cachexia, and other wasting disorders associated with chronic  
XX diseases. The nucleic acids and polypeptides may also be used as targets  
XX for the identification of small molecules that modulate or inhibit e.g.  
XX neurogenesis, cell differentiation, cell proliferation, haematopoiesis,  
XX wound healing and angiogenesis, in gene therapy, in generation of  
XX antibodies that bind immunospecifically to NOVX substances for use in  
XX therapeutic or diagnostic methods. The nucleic acids are further used as  
XX hybridisation probes, in chromosome mapping, tissue typing, preventive  
XX medicine, and pharmacogenomics. The polypeptides are also useful as  
XX vaccines. This is the amino acid sequence of a novel human G-protein  
XX coupled receptor related protein NOV  
SQ Sequence 644 AA;  
Query Match 90.0%; Score 618; DB 6; Length 644;  
Best Local Similarity 100.0%; Pred. No. 5.5e-62;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GKDFVQPTKICVCGPRDIPNPSPELEETLTHITKLNAENNAIFYKIDNVKARQV 62  
DB 253 GKDFVQPTKICVCGPRDIPNPSPELEETLTHITKLNAENNAIFYKIDNVKARQV 312  
QY 63 AGKYTFIDFVARETTCSKESNEELTESCETKKGQSLDCNAEYVVPPEKKIYPTV 118

Db 313 AGKVFIDFVARETTCESNEBELTESCETKLGQSLDCNAEVVYVPWEKKIYPTV 368

RESULT 15

AAB37447

ID AAB37447 standard; protein; 122 AA.

XX AC AAB37447;

XX DT 21-FEB-2001 (first entry)

XX DE Human kininogen D3.

XX KW Enzyme; legumain; endopeptidase; cystatin; human; kininogen.

XX OS Homo sapiens.

XX PN WO200064945-A1.

XX PD 02-NOV-2000.

XX PP 20-APR-2000; 2000WO-GB001571.

XX PR 22-APR-1999; 99GB-00009133.

XX PA (BADR-) BABRAHAM INST.

XX PI Abrahamson M, Barrett AJ;

XX DR WPI; 2000-687316/67.

XX PT Inhibition of mammalian legumain or legumain-related endopeptidase by cystatin involves interaction with second papain-non-reactive site of cystatin.

XX PS Disclosure; Fig 4; 45pp; English.

XX CC The present invention relates to inhibition of the enzymatic activity of legumain or a legumain-related endopeptidase by cystatin. The inhibition involves an interaction between legumain and a papain-non-reactive site of cystatin. Legumain (EC 3.4.22.34) is a cysteine endopeptidase, and performs a protein-processing function. The present sequence is human kininogen D3, which was used in the present invention. Kininogen is a type 3 cystatin

XX SQ Sequence 122 AA;

Query Match 85.3%; Score 586; DB 3; Length 122;

Best Local Similarity 100.0%; Pred. No. 2.7e-59;

Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 9 PPTKICVCCPRDPTSPLEBELTHTITKLAENNAATFYKIDNVKKARVOVWAGKKYP 68

DB 1 PPTKICVCCPRDPTSPLEBELTHTITKLAENNAATFYKIDNVKKARVOVWAGKKYP 60

OY 69 IDPVARETTCESNEBELTESCETKLGQSLDCNAEVVYVPWEKKIYPTV 118

DB 61 IDPVARETTCESNEBELTESCETKLGQSLDCNAEVVYVPWEKKIYPTV 110

Search completed: September 24, 2004, 14:08:38

Job time : 52.308 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 14:07:01 / Search time 14.732 Seconds  
(without alignments)  
445.051 Million cell updates/sec

Title: US-10-661-784-3

Perfect score: 687  
Sequence: 1 GSKGFVOPPKICVGCPRD.....VPWEKKIYPTTVVHNECF 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

- 1: /cgn2\_6/ptodata/2/iaa/5A.CONB.pdp.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B.CONB.pdp.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A.CONB.pdp.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B.CONB.pdp.\*
- 5: /cgn2\_6/ptodata/2/iaa/PTCUS.CONB.pdp.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pdp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description      |
|------------|-------|-------|--------|-------|------------------|
| 1          | 558   | 81.2  | 117    | 1     | US-08-193-114B-1 |
| 2          | 556.5 | 81.0  | 117    | 5     | PCT-US92-06809-1 |
| 3          | 153.5 | 23.8  | 145    | 2     | US-08-832-535-2  |
| 4          | 153.5 | 23.8  | 145    | 3     | US-09-015-485-2  |
| 5          | 153.5 | 23.8  | 145    | 3     | US-09-015-485-3  |
| 6          | 153.5 | 23.8  | 145    | 3     | US-09-431-480-9  |
| 7          | 153.5 | 23.8  | 145    | 3     | US-09-617-302-9  |
| 8          | 153.5 | 23.8  | 145    | 4     | US-09-528-436B-2 |
| 9          | 163   | 23.7  | 178    | 2     | US-08-791-522-1  |
| 10         | 163   | 23.7  | 178    | 3     | US-09-314-777-1  |
| 11         | 138.5 | 20.2  | 121    | 4     | US-09-775-932-14 |
| 12         | 138.5 | 20.2  | 128    | 4     | US-09-775-932-12 |
| 13         | 138.5 | 20.2  | 149    | 2     | US-08-461-030C-2 |
| 14         | 138.5 | 20.2  | 149    | 3     | US-08-744-138-2  |
| 15         | 138.5 | 20.2  | 149    | 3     | US-09-431-480-8  |
| 16         | 138.5 | 20.2  | 149    | 3     | US-09-431-480-10 |
| 17         | 138.5 | 20.2  | 149    | 3     | US-09-617-302-8  |
| 18         | 138.5 | 20.2  | 149    | 3     | US-09-617-302-10 |
| 19         | 138.5 | 20.2  | 149    | 4     | US-09-241-376-3  |
| 20         | 138.5 | 20.2  | 149    | 4     | US-09-940-497-2  |
| 21         | 137.5 | 20.0  | 112    | 4     | US-08-843-303-16 |
| 22         | 136.5 | 19.9  | 118    | 4     | US-09-775-932-24 |
| 23         | 135.5 | 19.7  | 146    | 6     | 5432264-6        |
| 24         | 134   | 19.5  | 148    | 5     | PCT-US95-07135-2 |
| 25         | 132.5 | 19.3  | 120    | 4     | US-09-775-932-2  |
| 26         | 132.5 | 19.3  | 145    | 2     | US-08-832-535-11 |
| 27         | 132.5 | 19.3  | 146    | 2     | US-08-791-522-3  |

|    |       |      |     |   |                   |
|----|-------|------|-----|---|-------------------|
| 28 | 132.5 | 19.3 | 146 | 3 | US-08-744-138-3   |
| 29 | 132.5 | 19.3 | 146 | 3 | US-09-019-485-4   |
| 30 | 132.5 | 19.3 | 146 | 3 | US-09-314-777-3   |
| 31 | 132.5 | 19.3 | 146 | 3 | US-09-431-480-6   |
| 32 | 132.5 | 19.3 | 146 | 3 | US-09-617-302-6   |
| 33 | 132.5 | 19.3 | 146 | 4 | US-09-241-376-3   |
| 34 | 132.5 | 19.3 | 146 | 4 | US-09-528-436B-3  |
| 35 | 132.5 | 19.3 | 146 | 4 | US-09-886-319A-47 |
| 36 | 132.5 | 19.3 | 146 | 4 | US-09-940-497-3   |
| 37 | 132.5 | 19.3 | 146 | 4 | US-09-976-594-37  |
| 38 | 132.5 | 19.3 | 146 | 4 | US-08-849-303-17  |
| 39 | 132.5 | 19.3 | 146 | 5 | PCT-US95-07135-9  |
| 40 | 132   | 19.2 | 26  | 3 | US-08-676-242-15  |
| 41 | 131.5 | 19.1 | 382 | 4 | US-09-599-160B-93 |
| 42 | 130   | 18.9 | 127 | 4 | US-08-849-303-13  |
| 43 | 129.5 | 18.9 | 140 | 4 | US-09-886-319A-46 |
| 44 | 129.5 | 18.9 | 140 | 4 | US-09-886-319A-48 |
| 45 | 128   | 18.6 | 111 | 4 | US-08-849-303-26  |

## ALIGNMENTS

### RESULT 1

US-08-193-114B-1  
Sequence 1, Application US/08193114B

Patent No. 5472945

GENERAL INFORMATION:

APPLICANT: Schmaier, Alvin H.

APPLICANT: Jiang, Yongping

TITLE OF INVENTION: Modulation of Blood

TITLE OF INVENTION: Pressure and Inhibition of Platelet Activation

TITLE OF INVENTION: with Kininogen Fragment

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seidel, Gonda, Lavorgna &

ADDRESSEE: Monaco, P.C.

STREET: 1800 Two Penn Center Plaza

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102

COMPUTER READABLE FORM: Diskette, 3.50 inch, 720 Kb

MEDIUM TYPE: IBM PS/2

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08193,114B

FILING DATE: 9 February 1994

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Application

APPLICATION NUMBER: Serial No. 5472945 07/744,545

FILING DATE: 13 August 1991

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, Daniel A.

REGISTRATION NUMBER: 30,480

REFERENCE/DOCKET NUMBER: 6056-137 CII

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

TELEX: No. 5472945e

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 117 amino acids

TYPE: peptide

TOPOLOGY: linear

US-08-193-114B-1

Query Match 81.2%; Score 558; DB 1; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2,38-55;  
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 CVGCPDIPNTPSPELBTHTITKLNAENNATFYKIDNVKARVQVWAGKKYFIDFVA 73  
 Db 1 CVGCPDIPNTPSPELBTHTITKLNAENNATFYKIDNVKARVQVWAGKKYFIDFVA 60  
 QY 74 RETTCSKESNEELTESCETKKGQSLDCNAEVVVPWEKKIYPTV 118  
 Db 61 RETTCSKESNEELTESCETKKGQSLDCNAEVVVPWEKKIYPTV 105

## RESULT 2

PCT-US92-06809-1  
 ; Sequence 1, Application PC/TUS9206809  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schmaier, Alvin H.  
 ; APPLICANT: Jiang, Yongping  
 ; TITLE OF INVENTION: Modulation of Blood  
 ; NUMBER OF INVENTION: Pressure by Altering Bradykinin Levels  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Temple University - Of the  
 ; STREET: 406 University System of Higher Education  
 ; CITY: Philadelphia  
 ; STATE: Pennsylvania  
 ; COUNTRY: U.S.A.  
 ; ZIP: 19122

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WordPerfect 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US92/06809  
 FILING DATE: 19910813  
 CLASSIFICATION: 514  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: U.S. Application  
 APPLICATION NUMBER: Serial No. 744,545  
 FILING DATE: 13 August 1991  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Monaco, Daniel A.  
 REGISTRATION NUMBER: 30,480  
 REFERENCE/DOCKET NUMBER: 6056-137  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (215) 568-8383  
 TELEFAX: (215) 568-5549  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 117 amino acids  
 TYPE: AMINO ACID  
 TOPOLOGY: linear

## PCT-US92-06809-1

Query Match 81.0%; Score 556.5; DB 5; Length 117;  
 Best Local Similarity 93.8%; Pred. No. 3.3e-55;  
 Matches 106; Conservative 1; Mismatches 1; Indels 5; Gaps 1;  
 QY 14 CVGCPDIPNTPSPELBTHTITKLNAENNATFYKIDNVKARVQVWAGKKYFIDFVA 73  
 Db 1 CVGCPDIPNTPSPELBTHTITKLNAENNATFYKIDNVKARVQVWAGKKYFIDFVA 60  
 QY 74 RETTCSKESNEELTESCETKKGQSLDCNAEVVVPWEKKIYPTV 126  
 Db 61 RETTCSKESNEELTESCETKKGQSLDCNAEVVVPWEKKIYPTV 108

## RESULT 3

US-08-832-535-2  
 ; Sequence 2, Application US/08812535  
 ; Patent No. 5919658

GENERAL INFORMATION:  
 APPLICANT: NI, JIAN  
 APPLICANT: LI, HAODONG  
 APPLICANT: YU, GUO-LIANG  
 APPLICANT: GENTZ, REINER L.  
 TITLE OF INVENTION: HUMAN CYSTATIN F  
 NUMBER OF SEQUENCES: 11  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
 STREET: 9410 KEY WEST AVENUE  
 CITY: ROCKVILLE  
 STATE: MD  
 COUNTRY: US  
 ZIP: 20850  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent in Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/832,535  
 FILING DATE: 03-APR-1997  
 CLASSIFICATION: 435  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KIMBALL, PAUL C.  
 REGISTRATION NUMBER: 34,610  
 REFERENCE/DOCKET NUMBER: PP265  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (201) 994-1700  
 TELEFAX: (201) 994-1744  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 145 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: Protein  
 US-08-832-535-2

Query Match 23.8%; Score 163.5; DB 2; Length 145;  
 Best Local Similarity 31.6%; Pred. No. 9.4e-11;  
 Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;  
 QY 11 TKICVGCPRDIPNTPSPELBTHTITKLNAENNATFYKIDNVKARVQVWAGKKYFID 70  
 Db 32 SRVKGPPPTXITNDPGVLAARYSVKFNCTNDMPFKESRITRALVQVGLKTMLE 91  
 QY 71 FVARETTCSSNEELTESCE---TKKLGQSLDCNAEVVVPWEKKIYPTVTVNHWE 124  
 Db 92 VEIGRTTCCKGQHLRL-DDCDFTQHTLXQTLSCYSEVMVVPW-----LQHEE 138

## RESULT 4

US-09-019-485-2  
 ; Sequence 2, Application US/09019485  
 ; Patent No. 6066617  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LI, Haodong  
 ; APPLICANT: Yu, Guo-Liang  
 ; APPLICANT: Gentz, Reiner  
 ; APPLICANT: NI, Jian  
 ; TITLE OF INVENTION: Cystatin F  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Human Genome Sciences, Inc.  
 ; STREET: 9410 Key West Avenue  
 ; CITY: Rockville  
 ; STATE: MD  
 ; COUNTRY: US  
 ; ZIP: 20850  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

```

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/019,485
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert H.
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: P285P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3013098504
TELEFAX: 3013098439
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-019-485-2

Query Match      23.8%   Score 163.5, DB 3,   Length 145,
Best Local Similarity 31.6%   Pred. No. 9,4e-11;
Matches 37, Conservative 22, Mismatches 45, Indels 13, Gaps 3;

QY      11 TKICVCPDDIDTNSPELEEELTHITIKLNAENNATPYEKIDNVKKARQVWAGKCYID 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      32 SRVKGPPKTIKTNDPGVLQARYSVEKFNNCTNDMFLFKESRITRALVOIVKGLKTMIE 91
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY      71 FVARETTCKSENEELTESCE---TKKLQSLDCNAAVYVVPWEKKIYPTVTVNHW 124
DB      92 VEIGRTTCKNGHSLR-DCDCFOTNNHTLKTGLTSCYSEVVVVVPM-----LQHPF 138
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 5  
 US-09-019-485-3  
 / Sequence 3, Application US/09019485  
 / Patent No. 6066617  
 / GENERAL INFORMATION:  
 / APPLICANT: Li, Haodong  
 / APPLICANT: Yu, Guo-Liang  
 / APPLICANT: Gentz, Reiner  
 / APPLICANT: Ni, Jian  
 / TITLE OF INVENTION: Cystatin F  
 / NUMBER OF SEQUENCES: 17  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSES: Human Genome Sciences, Inc.  
 / STREET: 9410 Key West Avenue  
 / CITY: Rockville  
 / STATE: MD  
 / COUNTRY: US  
 / ZIP: 20850  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: Patent In Release #1.0, Version #1.30  
 / CURRENT APPLICATION DATA:  
 / APPLICATION NUMBER: US/09/019,485  
 / FILING DATE:  
 / CLASSIFICATION:  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Benseon, Robert H.  
 / REGISTRATION NUMBER: 30,446  
 / REFERENCE/DOCKET NUMBER: P2665P1  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 3013098504  
 / TELEFAX: 3013098439  
 / INFORMATION FOR SEQ ID NO: 3:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 145 amino acids  
 / TYPE: amino acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear

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US-09-019-485-3
MOLECULE TYPE: protein
Query Match 23.8%; Score 163.5; DB 3; Length 145;
Best Local Similarity 31.6%; Pred. No. 9.4e-11;
Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;
QY 11 TKIVGCPDRIPNPSPELSEETLTHITKLNANNATPYFKIDNVKARVQVVGAKKYPID 70
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
32 SRVKGPPKTIKINDPGVLQAARYSVEKPNCTNDMLFKESRITRALVQIVKGLKYMLE 91
QY 71 FVARETTSKESNEELTESCE---TKGLQSLDCNABVYVVPWEKKIYPTVTNVHWE 124
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
92 VBIGRTTCKCKNOHLRL-DCDCPOTNHTLKQTLSCYSEVVVPPV-----LQHFE 138

RESULT 6
US-09-431-480-9
Sequence 9; Application US/09411480
Patent No. 6235708
GENERAL INFORMATION:
APPLICANT: Holloway, James L.
APPLICANT: Feldhaus, Andrew
TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
FILE REFERENCE: 98-72
CURRENT APPLICATION NUMBER: US/09/431,480
EARLIER FILING DATE: 1999-11-01
EARLIER APPLICATION NUMBER: 60/109,217
EARLIER FILING DATE: 1998-11-20
EARLIER APPLICATION NUMBER: 60/156,382
EARLIER FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 9
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
US-09-431-480-9
Query Match 23.8%; Score 163.5; DB 3; Length 145;
Best Local Similarity 31.6%; Pred. No. 9.4e-11;
Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;
QY 11 TKIVGCPDRIPNPSPELSEETLTHITKLNANNATPYFKIDNVKARVQVVGAKKYPID 70
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
32 SRVKGPPKTIKINDPGVLQAARYSVEKPNCTNDMLFKESRITRALVQIVKGLKYMLE 91
QY 71 FVARETTSKESNEELTESCE---TKGLQSLDCNABVYVVPWEKKIYPTVTNVHWE 124
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
92 VBIGRTTCKCKNOHLRL-DCDCPOTNHTLKQTLSCYSEVVVPPV-----LQHFE 138

```

```

RESULT 7
US-09-617-302-9
  Sequence 9, Application US/09617302
  Patent No. 6245529
  GENERAL INFORMATION:
  APPLICANT: Holloway, James L.
  APPLICANT: Felchhaus, Andrew
  TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T
  FILE REFERENCE: 98-72 C1
  CURRENT APPLICATION NUMBER: US/09/617,302
  CURRENT FILING DATE: 2000-07-17
  PRIOR APPLICATION NUMBER: 09/431,480
  PRIOR FILING DATE: 1999-11-01
  PRIOR APPLICATION NUMBER: 60/109,217
  PRIOR FILING DATE: 1998-11-20
  PRIOR APPLICATION NUMBER: 60/156,382
  PRIOR FILING DATE: 1999-09-28
  NUMBER OF SEQ ID NOS: 22
  SOFTWARE: FastSeq for Windows Version 3.0
  SEQ ID NO 9
  LENGTH: 145

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/ TYPE, PRT
/ ORGANISM: Homo sapiens
US-09-617-302-9

Query Match      23.8%; Score 163.5; DB 3; Length 145;
Best Local Similarity 31.6%; Pred. No. 9.4e-11;
Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;

QY 11 TKICVCPDPTNSPELETLTHITKLNAENNAATFYKIDNVKARVQVAGKYFID 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 32 SRVXGPPKTKTNDPGVLAARYSVKFNCTNDMPFKESRITRALVQIVKGLKYLE 91
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 71 FVARETTCKESNEELTESCE---TKQLQSLDCNAEYVVPWEKKIYPTVTNRWE 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 92 VEIGRTTCKNQHLRL-DDCDFQTNHTLKTLSYSEVWVVPW-----LQHPF 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
US-09-528-436B-2
/ Sequence 2, Application US/09528436B
/ Patent No. 6576745
/ GENERAL INFORMATION:
/ APPLICANT: LI, et al.
/ TITLE OF INVENTION: Human Cystatin P
/ FILE REFERENCE: PF265PDI1
/ CURRENT APPLICATION NUMBER: US/09/528,436B
/ PRIOR FILING DATE: 2000-03-17
/ PRIOR APPLICATION NUMBER: 09/019,485
/ PRIOR FILING DATE: 1998-01-29
/ PRIOR APPLICATION NUMBER: 08/832,535
/ PRIOR FILING DATE: 1999-04-03
/ PRIOR APPLICATION NUMBER: 60/014,795
/ PRIOR FILING DATE: 1996-04-03
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: Patent in version 3.2
/ SEQ ID NO 2
/ LENGTH: 145
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-528-436B-2

Query Match      23.8%; Score 163.5; DB 4; Length 145;
Best Local Similarity 31.6%; Pred. No. 9.4e-11;
Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;

QY 11 TKICVCPDPTNSPELETLTHITKLNAENNAATFYKIDNVKARVQVAGKYFID 70
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 32 SRVXGPPKTKTNDPGVLAARYSVKFNCTNDMPFKESRITRALVQIVKGLKYLE 91
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 71 FVARETTCKESNEELTESCE---TKQLQSLDCNAEYVVPWEKKIYPTVTNRWE 124
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 92 VEIGRTTCKNQHLRL-DDCDFQTNHTLKTLSYSEVWVVPW-----LQHPF 138
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 9
US-08-791-522-1
/ Sequence 1, Application US/08791522
/ Patent No. 5935817
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Goli, Suzya K.
/ TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
/ TITLE OF INVENTION: PROTEIN
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Incyte Pharmaceuticals, Inc.
/ STREET: 3174 Porter Drive
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: PASTSEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA: /09/314,777
/ APPLICATION NUMBER: US/09/314,777
/ FILING DATE:
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/791,522
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Billings, Lucy J.
/ REGISTRATION NUMBER: 36,749
/ REFERENCE/DOCKET NUMBER: PF-0193 US
```

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 178 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 IMMEDIATE SOURCE:  
 CLONE: 30443  
 US-09-314-777-1

Query Match 23.7%, Score 163, DB 3, Length 178,  
 Best Local Similarity 34.0%, Pred. No. 1.4e-10,  
 Matches 35, Conservative 20, Mismatches 44, Indels 4, Gaps 2;

Qy 11 TKICVGCPRDIPNTPNSPELEETLTHITKLNANNATPYFKIDNVKARVQVAGKKYPI 70  
 Db 54 SRVKGPPKTIKNDPGVLOARISVEKFNCTNDMPLEGRITRALVQIVKGLKTYMLE 113  
 Qy 71 FVARETTCSKESENEELTESCE---TKLGGSLDCNAEVVVPW 110  
 Db 114 VELGRITCKKQHLRL-DDCDFOINHTLKLTLSCYSEVWVWP 155

## RESULT 11

US-09-775-932-14;  
 Sequence 14, Application US/09775932

Patent No. 6534477

GENERAL INFORMATION:

APPLICANT: University of British Columbia

TITLE OF INVENTION: Production and use of Modified Cystatins

FILE REFERENCE: 58069

CURRENT APPLICATION NUMBER: US/09/775.932

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 1999-08-05

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 14

LENGTH: 121

TYPE: PRT

ORGANISM: Homo sapiens

US-09-775-932-14

Query Match 20.2%, Score 138.5, DB 4, Length 121,  
 Best Local Similarity 31.5%, Pred. No. 4.9e-08,  
 Matches 34, Conservative 22, Mismatches 45, Indels 7, Gaps 3;

Qy 10 PTKICVGCPRDIPNTPNSPELEETLTHITKLNANNATPYFKIDNVKARVQVAGKKYPI 69  
 Db 2 PGRMVGLRLDSPDPQVOKAAQAAVASYNMGSNIYYFRDTHIIKAQSLVAGIKYFL 61

Qy 70 DFVARETTCSKE-----SNEELTESCETKLGQ--SLDCNAEVVVPWE 111  
 Db 62 TMEMGSTDCRTRVGTGDHVDLT-TCPLAAGAQQEKLRCDFEVLVVPWQ 108

## RESULT 12

US-09-775-932-12

Sequence 12, Application US/09775932

Patent No. 6534477

GENERAL INFORMATION:

APPLICANT: University of British Columbia

TITLE OF INVENTION: Production and use of Modified Cystatins

FILE REFERENCE: 58069

CURRENT APPLICATION NUMBER: US/09/775.932

PRIOR FILING DATE: 2001-02-02

PRIOR FILING DATE: 1999-08-05

PRIOR APPLICATION NUMBER: 60/095,503

PRIOR FILING DATE: 1998-08-05

NUMBER OF SEQ ID NOS: 32

SOFTWARE: Patent in Ver. 2.0

SEQ ID NO 12

LENGTH: 128

TYPE: PRT

ORGANISM: Homo sapiens

US-09-775-932-12

Query Match 20.2%, Score 138.5, DB 4, Length 128,  
 Best Local Similarity 31.5%, Pred. No. 5.2e-08,  
 Matches 34, Conservative 22, Mismatches 45, Indels 7, Gaps 3;

Qy 10 PTKICVGCPRDIPNTPNSPELEETLTHITKLNANNATPYFKIDNVKARVQVAGKKYPI 69  
 Db 9 PGRMVGLRLDSPDPQVOKAAQAAVASYNMGSNIYYFRDTHIIKAQSLVAGIKYFL 68

Qy 70 DFVARETTCSKE-----SNEELTESCETKLGQ--SLDCNAEVVVPWE 111  
 Db 69 TMEMGSTDCRTRVGTGDHVDLT-TCPLAAGAQQEKLRCDFEVLVVPWQ 115

## RESULT 13

US-08-461-030C-2

Sequence 2, Application US/08461030C

Patent No. 5985601

GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: Yu, Guo-Liang

APPLICANT: Gentz, Reiner

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: Human Cystatin E

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Ave

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/461,030C

FILING DATE: 05-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: A. Anders, Brookes

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF202

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-301-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 149 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-461-030C-2

Query Match 20.2%, Score 138.5, DB 2, Length 149,  
 Best Local Similarity 31.5%, Pred. No. 6.4e-08,  
 Matches 34, Conservative 22, Mismatches 45, Indels 7, Gaps 3;

Qy 10 PTKICVGCPRDIPNTPNSPELEETLTHITKLNANNATPYFKIDNVKARVQVAGKKYPI 69  
 Db 30 PGRMVGLRLDSPDPQVOKAAQAAVASYNMGSNIYYFRDTHIIKAQSLVAGIKYFL 89



OY 70 DFVARETTCSKE-----SNEELTESCETKKGQ--SLDCNAEVVVPWE 111  
DB 90 TWENGSTDCRTRVTGDHVDLT-TCPLAAGAQOEKLRCDFEVLVVPWQ 136

## RESULT 14

US-08-744-138-2

Sequence 2, Application US/08744138

Patent No. 601012

GENERAL INFORMATION:

APPLICANT: Gentz, Reiner L.

APPLICANT: Ni, Jian

APPLICANT: Rosen, Craig A.

APPLICANT: Yu, Guo-Liang

TITLE OF INVENTION: Human Cystatin E

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

City: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/744,138

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF202P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301 309 8504

TELEFAX: 301 309 8512

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 149 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-744-138-2

Query Match 20.2%; Score 138.5; DB 3; Length 149;

Best Local Similarity 31.5%; Pred. No. 6.4e-08;

Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;

OY 10 PTKICVGCPRDIPNTPNSPELELTHTITKLAENNATFYFKIDNVKARVQVWAGKKYFI 69

DB 30 PQERNVGLRDLSPDDPQVQKAAQAAVASVYNGSNSIYYFRDTHIIKAQSQLVAGIKYFL 89

OY 70 DFVARETTCSKE-----SNEELTESCETKKGQ--SLDCNAEVVVPWE 111

DB 90 TWENGSTDCRTRVTGDHVDLT-TCPLAAGAQOEKLRCDFEVLVVPWQ 136

## RESULT 15

US-09-431-480-8

Sequence 8, Application US/09431480

Patent No. 6235708

GENERAL INFORMATION:

APPLICANT: Holloway, James L.

APPLICANT: Feldhaus, Andrew

TITLE OF INVENTION: TESTIS SPECIFIC CYSTATIN-LIKE PROTEIN CYSTATIN T

FILE REFERENCE: 98-72

CURRENT APPLICATION NUMBER: US/09/431,480

CURRENT FILING DATE: 1999-11-01

EARLIER APPLICATION NUMBER: 60/109,217

EARLIER FILING DATE: 1998-11-20

; EARLIER APPLICATION NUMBER: 60/156,382

; EARLIER FILING DATE: 1999-09-28

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 149

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-431-480-8

## Query Match

20.2%; Score 138.5; DB 3; Length 149;

Best Local Similarity 31.5%; Pred. No. 6.4e-08;

Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;

OY 10 PTKICVGCPRDIPNTPNSPELELTHTITKLAENNATFYFKIDNVKARVQVWAGKKYFI 69

DB 30 PQERNVGLRDLSPDDPQVQKAAQAAVASVYNGSNSIYYFRDTHIIKAQSQLVAGIKYFL 89

OY 70 DFVARETTCSKE-----SNEELTESCETKKGQ--SLDCNAEVVVPWE 111

DB 90 TWENGSTDCRTRVTGDHVDLT-TCPLAAGAQOEKLRCDFEVLVVPWQ 136

Search completed: September 24, 2004, 14:11:37

Job time : 15.732 sec



Anderson K.P., Croyle M.L., Lingrel J.B.;  
"Primary structure of a gene encoding rat T-kininogen.";  
Gene 91:119-128 (1989).

DR RA  
RT RL  
DR EMBL; M2090; AAA42251.1;  
DR EMBL; M2083; AAA42251.1; JOINED.  
DR EMBL; M2084; AAA42251.1; JOINED.  
DR EMBL; M2091; AAA42251.1; JOINED.  
DR EMBL; M2085; AAA42251.1; JOINED.  
DR EMBL; M2086; AAA42251.1; JOINED.  
DR EMBL; M2087; AAA42251.1; JOINED.  
DR EMBL; M2088; AAA42251.1; JOINED.  
DR EMBL; M2089; AAA42251.1; JOINED.  
DR PIR; S68034; S68034.  
DR PIR; S68035; S68035.  
DR GO; G00004869; Cysteine protease inhibitor activity; IEA.  
DR InterPro; IPR00010; Cystatin.  
DR Pfam; PF00031; cystatin; 1.  
DR SMART; SM00043; CY; 3.  
DR PROSITE; PS00287; CYSTATIN; 2.  
DR SEQ SEQUENCE 430 AA; 47618 MW; 45508DEF4BDC978C CRC64;

Query Match 55.0%; Score 378; DB 11; Length 430;  
Best Local Similarity 62.1%; Pred. No. 3,1e-29;  
Matches 72; Conservative 13; Mismatches 31; Indels 0; Gaps 0;

OY 3 GXDFVQPTKLCVCPRDIPHSPLRETLTHITTKLNENNAATPFVKIDNVKKARVWV 62  
DB 252 GDGLFSLPKRCRCRCPREIPTSPLKALGSHIAQLNQRHIFFKIDTVKKAATSOV 311

OY 63 AGKKVFDFVARETTCSSKNELTESCTKKLGCSLOCNAEYVVVWPEKKIYPTV 118  
DB 312 AGVIIVIEIARETNCSSKSTLTADCECHKLGSLNCANVMYMPRWENKVYPTV 367

RESULT 4  
OQ0ML5  
IID OQ0ML5 PRELIMINARY; PRS: 167 AA.

OC Q0M45  
DT 01-MAY-2000 (TREMBLrel\_13, Created)  
OC 01-MAY-2000 (TREMBLrel\_13, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel\_24, Last annotation update)  
GN Marine CHAP (CYSTATIN P) (LEUKOCYSTATIN).  
DE MARINE CHAP OR CST7.  
OS Mus musculus [Mouse].  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OC NBI\_TaxId=10090,  
RN [1]  
RR SEQUENCE FROM N.A.  
RR Morita M., Arakawa H., Yoshiuchi N.;  
RR "A novel cystatin-like metacaspase associated gene.";  
RR Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RR [2]

RR SEQUENCE FROM N.A.  
RR STRAIN=C57BL/6J; TISSUE=Embryo;  
RR MEDLINE=21085660; PubMedId=11217851;  
RR Kawaj J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RR Akawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RR Aizawa K., Izawa M., Nishi K., Kiyoawa H., Kondo S., Yananaka I.,  
RR Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RR Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RR Fleichmann W., Gaasterland T., Glenn C., King B., Kochiya H.,  
RR Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RR Schram L.M., Staebli F., Suzuki K., Tomita M., Wagner L., Washio T.,  
RR Blake J., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G.,  
RR Brownstein M.J., Bult C., Fletcher N., Carninci P., de Bonaldo M.F.,  
RR Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RR Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombarra P.,  
RR Nordone P., Ring B., Schoenbach C., Rodriguez I., Sakamoto N.,  
RR Sasaki H., Sato K., Ringswald M.C., Seya T., Shibata Y., Storch K.-P.,  
RR Suzuki H., Toyooka K., Wang X.H., Waltz C., Whittaker C., Wilming L.,  
RR Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontauki S.,

RA Hayaehizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL; AB015224, BAA34940.1, -;  
 DR ENBL; AK004420, BAB23298.1, -;  
 DR HSPF; P01034, IG96.  
 DR MGP; MGRI1298217, C87.  
 DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.  
 DR InterPro; IPR000010; Cystatin.  
 DR Pfam; PF00031; cystatin; 1.  
 DR SMART; SM00043; CY; 1.  
 SQ SEQUENCE 167 AA; 18847 MW; 61F776D8445095FE CRC64;

Query Match 25.0%; Score 171.5; DB 11; Length 167;  
 Best Local Similarity 35.5%; Pred. No. 3.4e-09;  
 Matches 39; Conservative 22; Mismatches 42; Indels 7; Gaps 3;

QY 4 KDPVQPTKICVCGCPDIPNPSPELETLTHTITKLAENNATFYFKIDNVKKARVQVVA 63  
 DB 50 KDIU---SSVKPGPRTKTETNPGLVAARSHVEKFNCTNDIFPKSHVSKALVQVX 106  
 QY 64 GKXYPIDPVARETTCKSKSNEELTESCE---TKKLGQSLDCNAEYVVPW 110  
 DB 107 GLKYMLEVKIGRTCKRKTMRQL-DNCDPQNPALKRTLYCYSEVWVWP 155

RESULT 5  
 Q724J8 PRELIMINARY; PRT; 167 AA.  
 AC Q724J8  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Cystatin P (leukocystatin).  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kalline N., Chen X., Rolfe A., Halleck A., Hines L., Eisenstein S.,  
 RA Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,  
 RA Phelan M., Farmer A.  
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BT009825, AAP08827.1, -;  
 SQ SEQUENCE 167 AA; 18857 MW; E339025A58D60177 CRC64;

Query Match 23.8%; Score 163.5; DB 4; Length 167;  
 Best Local Similarity 31.6%; Pred. No. 2.1e-08;  
 Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;

QY 11 TKICVCGCPDIPNPSPELETLTHTITKLAENNATFYFKIDNVKKARVQVVA 70  
 DB 54 SRVKPGPRTKTETNPGLVAARSHVEKFNCTNDIFPKSHVSKALVQVX 113  
 QY 71 FVARETTCKSKSNEELTESCE---TKKLGQSLDCNAEYVVPW 124  
 DB 114 VEIGRTCKKQNHRL-DNCDPQNPALKRTLYCYSEVWVWP-----LQHP 160

RESULT 6  
 Q72Y91 PRELIMINARY; PRT; 462 AA.  
 AC Q72Y91  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Similar to fetuin B.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 ON NCBI\_TaxID=8355;

RA SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA Klein S., Strauberg R.,  
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC043891, AAA43891.1, -;  
 DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.  
 DR InterPro; IPR000010; Cystatin.  
 DR Pfam; PF00031; cystatin; 2.  
 DR SMART; SM00043; CY; 2.  
 SQ SEQUENCE 462 AA; 53185 MW; D7BAD339961739FB CRC64;

Query Match 22.2%; Score 152.5; DB 13; Length 462;  
 Best Local Similarity 38.8%; Pred. No. 8.4e-07;  
 Matches 33; Conservative 13; Mismatches 34; Indels 5; Gaps 2;

QY 10 PTKICVCGCPDIPNPSPELETLTHT---ITKLAENNATFYFKIDNVKKARVQVVA 65  
 DB 142 PGVILSTCP-DCPTANEIPTITETADTLIAEYKDSNNTRYFKIDHIERVRSQWVGP 200  
 QY 66 KYPIQVARETTCKSKSNEELTESC 90  
 DB 201 SYPIQFTIKETDCMKTOENVLSNC 225

RESULT 7  
 Q7SVH2 PRELIMINARY; PRT; 462 AA.  
 AC Q7SVH2  
 DT 01-OCT-2003 (TRENBLrel. 25, Created)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Cystatin domain fetuin-like protein.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.  
 ON NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Ventral midgut;  
 RA Costa R.M.B., Mason J., Lee M., Amaya E., Zorn A.M.;  
 RA "Novel gene expression domains reveal early patterning of the Xenopus  
 RT endoderm."  
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY260732, AAP02289.1, -;  
 SQ SEQUENCE 462 AA; 53196 MW; 796P92774CC27721 CRC64;

Query Match 22.2%; Score 152.5; DB 13; Length 462;  
 Best Local Similarity 38.8%; Pred. No. 8.4e-07;  
 Matches 33; Conservative 13; Mismatches 34; Indels 5; Gaps 2;

QY 10 PTKICVCGCPDIPNPSPELETLTHT---ITKLAENNATFYFKIDNVKKARVQVVA 65  
 DB 142 PGVILSTCP-DCPTANEIPTITETADTLIAEYKDSNNTRYFKIDHIERVRSQWVGP 200  
 QY 66 KYPIQVARETTCKSKSNEELTESC 90  
 DB 201 SYPIQFTIKETDCMKTOENVLSNC 225

RESULT 8  
 Q801E5 PRELIMINARY; PRT; 465 AA.  
 AC Q801E5  
 DT 01-JUN-2003 (TRENBLrel. 24, Created)  
 DT 01-JUN-2003 (TRENBLrel. 24, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Hypothetical histidine-rich protein (fragment).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
 OC Xenopodinae; Xenopus.

```

OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=23480013; PubMed=12591597;
RA Chen Y., Jurgens K., Hollemann T., Claassen M., Ramadori G.,
RA Pieler T.,
RT "Cell-autonomous and signal-dependent expression of liver and
RT intestine marker genes in pluripotent precursor cells from xenopus
RT embryos.",
RL Mech. Dev. 120:277-288(2003).
DR EMBL: AY188284; AA031610.1; ..
DR GO: GO:0004869; P:cysteine protease inhibitor activity; IEA.
DR InterPro: IPR000010; Cystatin.
DR Pfam: PF00031; Cystatin; 2.
DR SMART: SM00043; CY; 2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 465 AA; 53528 MW; 0B403AB4P78BBFD4 CRC64;

Query Match 22.24; Score 152.5; DB 13; Length 465;
Best Local Similarity 38.84; Pred. No. 8.5e-07;
Matches 33; Conservative 13; Mismatches 34; Indels 5; Gaps 2;

OY 10 PTKICVCPDIPNTPSPELETLTHT---ITKLAENNAATFFKIDNVKARVOVWAGK 65
DB 145 PGVILSTCP-DCTANEELTPITETAEFLIAEYKDSNTRFKIDHIERVRSQWVGP 203

OY 66 KYPIDFVARETTCKESNEELTESC 90
DB 204 SYFIQTIKSTOCKTKOENVLNSC 228

RESULT 9
ID Q9EPX9 PRELIMINARY; PRT; 140 AA.
AC Q9EPX9,
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DR Cystatin C.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21010502; PubMed=11143350;
RA Taupin P.J., Ray J., Fischer W.H., Suhr S.T., Hakansson K., Grubb A.,
RA Gage P.H.;
RT "FGF-2-Responsive neural stem cell proliferation requires CCG, a novel
RT autocrine/paracrine cofactor.",
RL Neuron 28:385-397(2000).
DR EMBL: AF111741; AAC40283.1; ..
DR HSP: P01034; ICG6.
DR GO: GO:0004869; P:cysteine protease inhibitor activity; IEA.
DR InterPro: IPR000010; Cystatin.
DR Pfam: PF00031; Cystatin; 1.
DR SMART: SM00043; CY; 1.
DR PROSITE: PS00287; Cystatin; 1.
CHAIN 21 140 CYSTATIN C.
FT VARIAT 16 16 A -> G.
FT VARIANT 84 84 L -> P.
SQ SEQUENCE 140 AA; 15517 MW; 3A563406DD58D785 CRC64;

Query Match 19.14; Score 131.5; DB 11; Length 140;
Best Local Similarity 27.84; Pred. No. 2.6e-05;
Matches 32; Conservative 26; Mismatches 48; Indels 9; Gaps 4;

OY 15 VGCPRDIPNTPSPELETLTHTITKLAENNAATFFKIDNVKARVOVWAGKYPIDFVAR 74
DB 30 LGAPPEADANECCVRALDFAVSEYNKGSNDAYHSRAIQVVRKQLVAGVNYFLDVMG 89

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OY 75 ETTCKESNEELTESC---ETKKGQSLDCAEAVVVPWEKKIYPTVTNWECE 126
DB 90 RTTCTK-SQTNLTD-CPPHDQPHLMKALCSFOIYSPWK----GTHSLTNPSCK 138

RESULT 10
ID Q800S8 PRELIMINARY; PRT; 455 AA.
AC Q800S8,
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DR Fetuin-A.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Jia F.;
RT "Danio rerio fetuin-A",
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY217758; AA061483.1; ..
DR GO: GO:0005874; C:microtubule; IEA.
DR GO: GO:0004869; P:cysteine protease inhibitor activity; IEA.
DR GO: GO:0005198; P:structural molecule activity; IEA.
DR GO: GO:0007018; P:microtubule-based movement; IEA.
DR InterPro: IPR002453; Beta tubulin.
DR InterPro: IPR000010; Cystatin.
DR Pfam: PF00031; Cystatin; 1.
DR SMART: SM00043; CY; 1.
DR PROSITE: PS00228; TUBULIN B AUTOREG; 1.
SQ SEQUENCE 455 AA; 50627 MW; D822872926BAJACB CRC64;

Query Match 18.04; Score 123.5; DB 13; Length 455;
Best Local Similarity 26.74; Pred. No. 0.00063;
Matches 32; Conservative 23; Mismatches 46; Indels 19; Gaps 4;

OY 2 SGDFVQPTTKICVCPDIPNTPSPELETLTHTITKLAENNAATFFKIDNVKARVQ- 60
DB 134 SHEDLV---KKCPDCGGLFLHPEPKALSVNAALAKFKSNHKSYPKLMHVGRISSQW 189

OY 61 VVAGKYPIDFVARETTCKESNEELTESC---CETKKG-OSLDCNAEY 106
DB 190 MPMGOSYPTQFAIMETNCTKKDAPQNPPEACKALCGDQATYGFCKSKVSGSEPECEIY 249

RESULT 11
ID Q8CB17 PRELIMINARY; PRT; 388 AA.
AC Q8CB17,
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DR Fetuin beta.
GN FETUB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Vagina;
RX MEDLINE=22354883; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.",
RL Nature 420:563-573(2002).
DR EMBL: AK037043; BAC29682.1; ..
DR MGI: 1890221; Fetub.

```



RP SEQUENCE FROM N.A.  
RC TISSUE=estricle;  
RA Strausberg R.  
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC048646; AAH48646.1; -  
DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.  
DR InterPro; IPR000010; Cystatin.  
DR InterPro; IPR003243; Cystatin\_C/M.  
DR Pfam; PF00031; cystatin; 1.  
DR ProDom; PD001231; Cystatin\_C/M; 1.  
DR SMART; SM00043; CY; 1.  
SQ SEQUENCE 140 AA; 16199 MW; 32633299C4697DA0 CRC64;

Query Match 16.4%; Score 113; DB 11; Length 140;  
Best Local Similarity 29.4%; Pred. No. 0.0018;  
Matches 25; Conservative 18; Mismatches 38; Indels 4; Gaps 2;

QY 28 LEETLITITIKLAENNATPYKIDNVKARVQVAGKKYFIDFVARETTCSKESNELT 87  
DB 44 INSTLHPFIRSYNASNDTYLYQVQKLIQGMQLTGVYLVTVYKIGRTCKK--NETKK 101  
QY 88 ESC--ETKQLGQSLDCNAEVVVPW 110  
DB 102 ASCLQSSKLKSLICKSLIYSVPW 126

RESULT 15  
QY 08K397 PRELIMINARY; PRT; 146 AA.  
AC 08K397,  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE RIKEN CDNA 110017811 gene (fragment).  
OC Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Mammary gland;  
RA Strausberg R.  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC027680; AAH27680.1; -  
DR GO; GO:0004869; F:cysteine protease inhibitor activity; IEA.  
DR InterPro; IPR000010; Cystatin.  
DR Pfam; PF00031; cystatin; 1.  
DR SMART; SM00043; CY; 1.  
PT NON TER 1  
SQ SEQUENCE 146 AA; 16380 MW; 9D77BB9A6063A5C4 CRC64;

Query Match 16.2%; Score 111; DB 11; Length 146;  
Best Local Similarity 30.5%; Pred. No. 0.003;  
Matches 29; Conservative 18; Mismatches 42; Indels 6; Gaps 4;

QY 22 PTHSPLESELTITIKLAENNATPYKIDNVKARVQVAGKKYFIDFVARETTCSKE 81  
DB 40 PTD-PRVQAQAQAAVASTMGSDSLYPRDTKVIDAKYLVAGIKYLLDLIESTCKRT 98  
QY 82 --SNEEL-TESCETKILQ--SLDCNAEVVVPWE 111  
DB 99 RVSGEHMDLTTCPLAAGGQOEKRCNPELLEVPWK 133

Search completed: September 24, 2004, 14:10:18  
Job time : 37.576 secs



GenCore version 5.1.6  
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OK protein - protein search, using sw model

Run on: September 24, 2004, 14:04:32 ; Search time 8.636 seconds  
(without alignment)  
765.738 Million cell updates/sec

Title: US-10-661-784-3

Perfect score: 687

Sequence: 1 GSGKDFVGPPTKICVGCPRD.....VPWEKKIYPTVTNHWCEP 127

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 04

Maximum Match 1004

Listing first 45 summaries

Database : SwissProt\_42.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-------------|
| 1          | 618   | 90.0        | 644    | 1     | KNG_HUMAN   |
| 2          | 440   | 64.0        | 644    | 1     | KXLI_BOVIN  |
| 3          | 440   | 64.0        | 621    | 1     | KXLI_BOVIN  |
| 4          | 413   | 60.1        | 619    | 1     | KXLI_BOVIN  |
| 5          | 413   | 60.1        | 619    | 1     | KXLI_BOVIN  |
| 6          | 413   | 60.1        | 661    | 1     | KNG_MOUSE   |
| 7          | 410   | 59.7        | 639    | 1     | KNG_RAT     |
| 8          | 388   | 56.5        | 639    | 1     | KNT2_RAT    |
| 9          | 380   | 55.3        | 430    | 1     | KNT1_RAT    |
| 10         | 171.5 | 25.0        | 144    | 1     | CYTF_MOUSE  |
| 11         | 163.5 | 23.8        | 145    | 1     | CYTF_HUMAN  |
| 12         | 138.5 | 20.2        | 146    | 1     | CYTC_MACMU  |
| 13         | 138.5 | 20.2        | 149    | 1     | CYTM_HUMAN  |
| 14         | 137.5 | 20.0        | 148    | 1     | CYTC_BOVIN  |
| 15         | 135   | 19.7        | 378    | 1     | FETB_RAT    |
| 16         | 132.5 | 19.3        | 146    | 1     | CYTC_HUMAN  |
| 17         | 132.5 | 19.3        | 146    | 1     | CYTC_SALISC |
| 18         | 131.5 | 19.1        | 382    | 1     | FETB_HUMAN  |
| 19         | 130   | 18.9        | 127    | 1     | CYTC_RAT    |
| 20         | 129.5 | 18.9        | 140    | 1     | CYTC_MOUSE  |
| 21         | 128   | 18.6        | 111    | 1     | CYT_BITAR   |
| 22         | 124.5 | 18.1        | 141    | 1     | CYTI_HUMAN  |
| 23         | 124.5 | 18.1        | 148    | 1     | CYTI_RABIT  |
| 24         | 122.5 | 17.8        | 116    | 1     | CYT_COTJA   |
| 25         | 119   | 17.3        | 388    | 1     | FETB_MOUSE  |
| 26         | 118.5 | 17.2        | 139    | 1     | CYT_CHICK   |
| 27         | 113   | 16.4        | 141    | 1     | CYTS_RAT    |
| 28         | 109.5 | 15.9        | 141    | 1     | CYTN_HUMAN  |
| 29         | 108.5 | 15.8        | 141    | 1     | CYTS_HUMAN  |
| 30         | 107   | 15.6        | 130    | 1     | CYT_ONCKS   |
| 31         | 105.5 | 15.4        | 162    | 1     | CYTX_ONCVO  |
| 32         | 105   | 15.3        | 130    | 1     | CYT_ONCKY   |
| 33         | 104   | 15.1        | 129    | 1     | CYT_CYPCA   |

#### RESULT 1

| ID | KNG_HUMAN   | STANDARD | PRT | 644 AA |
|----|---|----------|-----|--------|
| AC | P01042, P01043  |          |     |        |
| DT | 21-JUL-1986 (Rel. 01, Created)  |          |     |        |
| DT | 01-FEB-1996 (Rel. 33, Last sequence update)   |          |     |        |
| DT | 10-OCT-2003 (Rel. 42, Last annotation update)   |          |     |        |
| DE | Kinogen precursor (Alpha-2-thiol proteinase inhibitor) [Contains: Bradykinin]   |          |     |        |
| GN | KNG   |          |     |        |
| OS | Homo sapiens (Human)  |          |     |        |
| OC | Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  |          |     |        |
| OX | NCBI_TaxID=9606   |          |     |        |
| RN | [1]   |          |     |        |
| RP | SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).  |          |     |        |
| RC | TISSUE=Liver  |          |     |        |
| EX | MEDLINE=85234582; PubMed=2989293  |          |     |        |
| RA | Takagaki Y., Kitamura N., Nakanishi S.  |          |     |        |
| RT | "Cloning and sequence analysis of cDNAs for human high molecular weight and low molecular weight prekininogens. Primary structures of two human prekininogens." |          |     |        |
| RL | J. Biol. Chem. 260:8601-8609(1985).   |          |     |        |
| RN | [2]   |          |     |        |
| RP | GENE STRUCTURE.   |          |     |        |
| EX | MEDLINE=85234583; PubMed=2989294  |          |     |        |
| RA | Kitamura N., Kitagawa H., Fukushima D., Takagaki Y., Miyata T., Nakanishi S.  |          |     |        |
| RT | "Structural organization of the human kininogen gene and a model for its evolution."  |          |     |        |
| RL | J. Biol. Chem. 260:8610-8617(1985).   |          |     |        |
| RN | [3]   |          |     |        |
| RP | SEQUENCE OF 1-401 FROM N.A.   |          |     |        |
| EX | MEDLINE=85122621; PubMed=6441591  |          |     |        |
| RA | Okubo I., Kurachi K., Takasawa T., Shikawa H., Sasaki M.,   |          |     |        |
| RT | "Isolation of a human cDNA for alpha 2-thiol proteinase inhibitor and its identity with low molecular weight kininogen."  |          |     |        |
| RL | Biochemistry 23:5691-5697(1984).  |          |     |        |
| RN | [4]   |          |     |        |
| RP | SEQUENCE OF 379-644.  |          |     |        |
| EX | MEDLINE=86030270; PubMed=4054110  |          |     |        |
| RA | Lottspeich F., Kellermann J., Henschen A., Foerster B., Mueller-Eberhard W.   |          |     |        |
| RT | "The amino acid sequence of the light chain of human high-molecular-mass kininogen."  |          |     |        |
| RL | Eur. J. Biochem. 152:307-314(1985).   |          |     |        |
| RN | [5]   |          |     |        |
| RP | SEQUENCE OF 381-389.  |          |     |        |
| EX | MEDLINE=90255622; PubMed=4952632  |          |     |        |
| RA | Pierce J.V.   |          |     |        |
| RT | "Structural features of plasma kinins and kininogens."  |          |     |        |
| RL | Fed. Proc. 27:52-57(1968).  |          |     |        |
| RN | [6]   |          |     |        |
| RP | DISULFIDE BONDS.  |          |     |        |
| RA | Sueyoshi T., Miyata T., Kato H., Iwanaga S.   |          |     |        |
| RT | "Disulfide bonds in bovine HMW kininogens."   |          |     |        |

|    |      |      |     |   |            |
|----|------|------|-----|---|------------|
| 34 | 102  | 14.8 | 122 | 1 | CYTA_SARPE |
| 35 | 101  | 14.7 | 139 | 1 | CS11_MOUSE |
| 36 | 95   | 13.8 | 165 | 1 | CSTL_HUMAN |
| 37 | 94.5 | 13.8 | 142 | 1 | CSTL_MOUSE |
| 38 | 94.5 | 13.8 | 345 | 1 | A2HS_MOUSE |
| 39 | 94   | 13.7 | 142 | 1 | CSTL_HUMAN |
| 40 | 93   | 13.5 | 99  | 1 | CYT_NAJAT  |
| 41 | 93   | 13.5 | 137 | 1 | CS11_HUMAN |
| 42 | 93   | 13.5 | 142 | 1 | CYTD_HUMAN |
| 43 | 91.5 | 13.3 | 135 | 1 | CYTI_MALZE |
| 44 | 91.5 | 13.3 | 352 | 1 | A2HS_RAT   |
| 45 | 88   | 12.8 | 367 | 1 | A2HS_HUMAN |

#### ALIGNMENTS

P31727 sarcophaga  
Q9d269 mus musculus  
Q9h114 homo sapien  
P31766 mus musculus  
P39699 mus musculus  
O60676 homo sapien  
P81714 naia atra  
Q9h112 homo sapien  
P38335 homo sapien  
P31766 mus musculus  
P24090 rattus norv  
P02765 homo sapien



21-JUL-1986 (Rel. 01, Last sequence update)  
 15-MAR-2004 (Rel. 43, Last annotation update)  
 Kininogen, LMW I precursor (Thiol proteinase inhibitor) (Contains:  
 Bradykinin).  
 Bos taurus (Bovine).  
 Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 Bovidae; Bovinae; Bos.  
 NCBI\_Taxid=9913;  
 [1]  
 SEQUENCE FROM N.A.  
 MEDLINE=83117859; PubMed=4572010;  
 Nawa H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S.,  
 "Primary structures of bovine liver low molecular weight kininogen  
 precursors and their two mRNAs.",  
 Proc. Natl. Acad. Sci. U.S.A. 80:90-94 (1983).  
 [2]  
 SEQUENCE OF 19-378.  
 MEDLINE=87137530; PubMed=3546295;  
 Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,  
 Miyata T., Iwanaga S.,  
 "Bovine high molecular weight kininogen. The amino acid sequence,  
 positions of carbohydrate chains and disulfide bridges in the heavy  
 chain portion.",  
 J. Biol. Chem. 262:2768-2779 (1987).  
 RL  
 J. Biol. Chem. 262:2768-2779 (1987).  
 CC  
 -1- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)  
 LMW-kininogen inhibits the aggregation of thrombocytes; (3) the  
 active peptide kallidin that is released from LMW-kininogen shows  
 a variety of physiological effects; (3A) influence in smooth  
 muscle contraction, (3B) induction of hypotension, (3C)  
 natriuresis and diuresis (kidney).  
 CC  
 -1- SUBCELLULAR LOCATION: Extracellular.  
 CC  
 -1- ALTERNATIVE PRODUCTS:  
 CC  
 Event=alternative splicing; Named isoforms=2;  
 CC  
 Name=LMW I; Sequence=Displayed;  
 CC  
 IsoId=IP01046-1; Sequence=Displayed;  
 CC  
 Name=HMW I;  
 CC  
 IsoId=IP01044-1; Sequence=External;  
 CC  
 -1- TISSUE SPECIFICITY: Plasma.  
 CC  
 -1- PTM: Bradykinin is released from kininogen by plasma kallikrein.  
 CC  
 -1- MISCELLANEOUS: LMW-kininogen is in contrast to HMW-kininogen not  
 involved in blood clotting.  
 CC  
 -1- SIMILARITY: Contains 3 cystatin-like domains.  
 CC  
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 or send an email to [license@ebi-sib.ch](mailto:license@ebi-sib.ch).  
 CC  
 EMBL; V00426; CAA23709.1; .  
 DR  
 PIR; A01283; KGBOL1.  
 DR  
 InterPro; IPR000010; Cystatin.  
 DR  
 Pfam; PF00031; cystatin; 3.  
 DR  
 SMART; SM00043; CV; 3.  
 DR  
 PROSITE; PS00287; CYSTATIN; 2.  
 KW  
 Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;  
 KW  
 Thiol protease inhibitor; Bradykinin; Signal;  
 KW  
 Pyroglutamate carboxylic acid.  
 FT  
 SIGNAL 1 18  
 FT  
 CHAIN 19 436 KININOGEN, LMW I.  
 FT  
 CHAIN 19 378 HEAVY CHAIN.  
 FT  
 PEPTIDE 380 388 BRADYKININ.  
 FT  
 CHAIN 389 436 LIGHT CHAIN.  
 FT  
 DOMAIN 19 135 CYSTATIN-LIKE 1.  
 FT  
 DOMAIN 136 257 CYSTATIN-LIKE 2.  
 FT  
 DOMAIN 258 378 CYSTATIN-LIKE 3.  
 FT  
 MOD RES 19 19 PYRROLIDONE CARBOXYLIC ACID.  
 FT  
 MOD RES 87 87 N-LINKED (GLCNAC. . .).  
 FT  
 CARBOHYD 136 136 O-LINKED (PARTIAL. . .).  
 FT  
 CARBOHYD 168 168 N-LINKED (GLCNAC. . .) (OR 169).

FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (PARTIAL. . .).  
 FT CARBOHYD 204 204 N-LINKED (GLCNAC. . .).  
 FT DISULFID 27 406 INTERCHAIN.  
 FT DISULFID 82 93  
 FT DISULFID 106 125  
 FT DISULFID 141 144  
 FT DISULFID 205 217  
 FT DISULFID 228 247  
 FT DISULFID 263 266  
 FT DISULFID 327 339  
 FT DISULFID 350 369  
 FT CONFLICT 295 295  
 FT SEQUENCE 436 AA; 48427 MW; P01F7B86814BCE6C CRC64;  
 SO  
 Query Match 54.0%; Score 440; DB 1; Length 436;  
 Best Local Similarity 70.4%; Pred. No. 1.8e-34;  
 Matches 81; Conservative 14; Mismatches 20; Indels 0; Gaps 0;  
 QY 4 KDPVQPTKICVCGPRDIPFNSEPELEETITHTITKLNANNATFYKIDNVKKARVQVVA 63  
 DB 253 KDPVQPTKICVCGPRDIPFNSEPELEETITHTITKLNANNATFYKIDNVKKARVQVVA 312  
 QY 64 GKYPIDPVARETTCSEKNEELTSCETKKGSLDCNARFVYVVPWEKKIYPTV 118  
 DB 313 GKYSIVFIARETTCSKSGNEELTKSCINITHQILHCDANVYVVPWEKKIYPTV 367  
 RESULT 3  
 ID KHHI BOVIN STANDARD; PRT; 621 AA.  
 AC P01044;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Kininogen, HMW I precursor (Thiol proteinase inhibitor) (Contains:  
 Bradykinin).  
 DE Bos taurus (Bovine).  
 OC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OK NCBI\_Taxid=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=84014106; PubMed=6571699;  
 RA Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., Nakanishi S.,  
 "A single gene for bovine high molecular weight and low molecular  
 weight kininogens.",  
 Nature 305:545-549 (1983).  
 RL Nature 305:545-549 (1983).  
 RN [2]  
 RP SEQUENCE OF 19-378.  
 RX MEDLINE=87137530; PubMed=3546295;  
 RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H.,  
 Miyata T., Iwanaga S.,  
 "Bovine high molecular weight kininogen. The amino acid sequence,  
 positions of carbohydrate chains and disulfide bridges in the heavy  
 chain portion.",  
 J. Biol. Chem. 262:2768-2779 (1987).  
 RL J. Biol. Chem. 262:2768-2779 (1987).  
 RN [3]  
 RP SEQUENCE OF 378-393.  
 RX MEDLINE=70180420; PubMed=4986212;  
 RA Kato H., Nagasawa S., Suzuki T.,  
 "Studies on the structure of bovine kininogen: cleavages of disulfide  
 bonds and of methionyl bonds in kininogen-II.",  
 J. Biochem. 67:313-323 (1970).  
 RL J. Biochem. 67:313-323 (1970).  
 RN [4]  
 RP SEQUENCE OF 458-498.  
 RX MEDLINE=75170265; PubMed=1169237;  
 RA Han Y.N., Komaya M., Iwanaga S., Suzuki T.,  
 "Studies on the primary structure of bovine high-molecular-weight  
 kininogen. Amino acid sequence of a fragment ('histidine-rich  
 peptide') released by plasma kallikrein.",  
 J. Biochem. 77:55-68 (1975).  
 RL J. Biochem. 77:55-68 (1975).  
 CC -1- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)

HMW-kininogen plays an important role in blood coagulation by helping to position optimally prekallikrein and factor XI next to factor XII; (3) HMW-kininogen inhibits the thrombin- and plasmin-induced aggregation of thrombocytes; (4) the active peptide bradykinin that is released from HMW-kininogen shows a variety of physiological effects: (4A) influence in smooth muscle contraction, (4B) induction of hypotension, (4C) natriuresis and diuresis, (4D) decrease in blood glucose level, (4E) it is a mediator of inflammation and causes (4E1) increase in vascular permeability, (4E2) stimulation of nociceptors (4E3) release of other mediators of inflammation (e.g. prostaglandins), (4F) it has a cardioprotective effect (directly via bradykinin action, indirectly via endothelium-derived relaxing factor action).

-1- SUBCELLULAR LOCATION: Extracellular.

-1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=HMW I;

Isoid=P01044-1; Sequence=Displayed;

Name=HMW I;

Isoid=P01046-1; Sequence=External;

-1- TISSUE SPECIFICITY: Plasma

-1- PTM: Bradykinin is released from kininogen by plasma kallikrein.

-1- SIMILARITY: Contains 3 Cystatin-like domains.

-----

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-----

EMBL: V01491; CAA24735.1; ..

PIR: A01281; KGBOL1.

InterPro: IPR000010; Cystatin.

InterPro: IPR002395; Kininogen.

Pfam: PF00033; Cystatin; 3.

PRINTS: PR00334; KININOGEN.

SMART: SM00043; CY, 3.

PROSITE: PS00287; CYSTATIN; 2.

Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;

Thiol protease inhibitor; Bradykinin; Blood coagulation;

Inflammatory response; Signal; Pyrrolidone carboxylic acid.

SIGNAL 1 18 PROBABLE.

CHAIN 19 621 KININOGEN, HMW I.

CHAIN 19 378 HEAVY CHAIN.

PT PEPTIDE 380 388 BRADYKININ.

PT CHAIN 389 621 LIGHT CHAIN.

PT DOMAIN 19 135 CYSTATIN-LIKE 1.

PT DOMAIN 126 257 CYSTATIN-LIKE 2.

PT DOMAIN 258 378 CYSTATIN-LIKE 3.

MOD\_RES 19 19 PYRROLIDONE CARBOXYLIC ACID.

PT CARBOHYD 87 87 N-LINKED (GLCNAC. . .).

PT CARBOHYD 136 136 O-LINKED (PARTIAL. . .).

PT CARBOHYD 168 168 N-LINKED (GLCNAC. . .).

PT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (OR 169).

PT CARBOHYD 204 204 N-LINKED (GLCNAC. . .) (PARTIAL).

PT DISULFID 27 591 INTERCHAIN.

PT DISULFID 87 93

PT DISULFID 106 125

PT DISULFID 141 144

PT DISULFID 205 217

PT DISULFID 228 247

PT DISULFID 263 266

PT DISULFID 327 339

PT DISULFID 350 369

SEQUENCE 621 AA; 68890 MW; D16850BEFE3C55CD CRC64;

Query Match 64.0%; Score 440; DB 1; Length 621;

Best Local Similarity 70.4%; Pred. No. 2.7e-34;

Matches 81; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

4 KDFVQPTKLCVGPDIPTNSPELEETLTHITKLNAENATFFKIDNVKARVQVVA 63

DB 253 KDFVQPTKLCVGPDIPTNSPELEETLTHITKLNAENATFFKIDNVKARVQVVA 312

QY 64 GKXVPTDFVARETTCKSNBELTSETCKLGLSGLDCAVYVYVPEKVIPTV 118

DB 313 GLKYSIVPARETTCKSNBELTSETCKLGLSGLDCAVYVYVPEKVIPTV 367

-----

RESULT 4

KNL2\_BOVIN

ID KNL2\_BOVIN STANDARD; PRT; 434 AA.

AC P01047;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Kininogen, LMW II precursor (Thiol proteinase inhibitor) (Contains: Bradykinin)

DE Bos taurus (Bovine).

OS Bos taurus (Bovine).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos.

OX NCBI\_TaxID:9913;

RN [1]

RP SEQUENCE FROM N.A.

RP MEDLINE=83117859; PubMed=6572010;

RA Nava H., Kitamura N., Hirose T., Asai M., Inayama S., Nakanishi S., "Primary structures of bovine liver low molecular weight kininogen precursors and their two mRNAs.", Proc. Natl. Acad. Sci. U.S.A. 80:190-94 (1983).

RN [2]

RP SEQUENCE OP 19-376

RP MEDLINE=87137530; PubMed=3546295;

RA Sueyoshi T., Miyata T., Hashimoto N., Kato H., Hayashida H., Miyata T., Iwanaga S.; "Bovine high molecular weight kininogen. The amino acid sequence, positions of carbohydrate chains and disulfide bridges in the heavy chain portion.", J. Biol. Chem. 262:2768-2779 (1987).

CC -1- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2) LMW-kininogen inhibits the aggregation of thrombocytes; (3) the active peptide kallidin that is released from LMW-kininogen shows a variety of physiological effects: (3A) influence in smooth muscle contraction, (3B) induction of hypotension, (3C) natriuresis and diuresis (kidney).

CC -1- SUBCELLULAR LOCATION: Extracellular.

CC -1- ALTERNATIVE PRODUCTS:

Event=Alternative splicing; Named isoforms=2;

Name=LMW II;

Isoid=P01047-1; Sequence=Displayed;

Name=HMW II;

Isoid=P01045-1; Sequence=External;

-1- TISSUE SPECIFICITY: Plasma.

-1- PTM: Bradykinin is released from kininogen by plasma kallikrein.

-1- MISCELLANEOUS: LMW-kininogen is in contrast to HMW-kininogen not involved in blood clotting.

-1- SIMILARITY: Contains 3 Cystatin-like domains.

-----

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EMBL: V00427; CAA23710.1; ..

PIR: A01284; KGBOL2.

HGSP: P01038; 1A90.

InterPro: IPR000010; Cystatin.

Pfam: PF00031; Cystatin; 3.

SMART: SM00043; CY, 3.

PROSITE: PS00287; CYSTATIN; 2.

Glycoprotein; Plasma; Repeat; Vasodilator; Alternative splicing;

SEQUENCE OF 376-391.

PT DOMAIN 257 376  
 MOD\_RES 19 19  
 CARBOHYD 87 87  
 CARBOHYD 136 136  
 CARBOHYD 168 168  
 CARBOHYD 197 197  
 CARBOHYD 204 204  
 CARBOHYD 280 280  
 CARBOHYD 400 400  
 DISULFID 27 589  
 DISULFID 82 93  
 DISULFID 106 125  
 DISULFID 141 144  
 DISULFID 205 217  
 DISULFID 228 247  
 DISULFID 261 264  
 DISULFID 325 337  
 DISULFID 348 367  
 VARIANT 398 398  
 VARIANT 401 401  
 VARIANT 454 454  
 SEQUENCE 619 AA, 68710 MW, P04320ABE0E0DA CRC64;  
 Query Match 60.1%; Score 413; DB 1; Length 619;  
 Best Local Similarity 67.2%; Pred. No. 9.9e-32;  
 Matches 78; Conservative 14; Mismatches 22; Indels 2; Gaps 1;  
 QY 3 GNDVFPPTKICVCPDIPNPSLEELTHITKLAENNAFFPKIDNVKARVQV 62  
 DB 252 GEDEL-PPMVCVCPKPIVDSPDLLEALNHSIAKLNAEHDGTFYFKIDTVKATVQV 309  
 QY 63 AGKQYDFDFARETTCKSENELTESCTKLGOSLDCNAEVVVPWEKKYPTV 118  
 DB 310 GGLKYSIVFIARETTCKSNEELTKSEINHGQILHCDNVVVPWEKKYPTV 365  
 RESULT 6  
 KNG\_MOUSE STANDARD; PRT; 661 AA.  
 AC O08677; O08676; OS1XKS;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Kininogen precursor [Contains: Bradykinin].  
 GN KNG.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBI\_TaxID=10090;  
 [1]\_TaxID=10090;  
 RP SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).  
 RC STRAIN=C57BL/6 X CBA; TISSUE=Liver;  
 RX MEDLINE=97343556; PubMed=9199253;  
 RA Takano M., Kondo J., Yayama K., Okani M., Sano K., Okamoto H.;  
 RT "Molecular cloning of cDNAs for mouse low-molecular-weight and high-  
 RT molecular-weight prekallikrogens.";  
 RL Biochim. Biophys. Acta 1352:222-230 (1997).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM LMW).  
 RC STRAIN=C57BL/6J; TISSUE=Placenta;  
 RX MEDLINE=23354683; PubMed=12466851;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
 RA Naka K., Tomaru Y., Hasegawa Y., Nogi A., Schorbach C., Gojibori T.,  
 RA Baldairelli R., Hill D.P., Bult C., Rume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
 RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Fraser K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,

RA Nageshima T., Numata K., Okido T., Pavan W.J., Perlea G., Pesole G.,  
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sandelin A., Schneider C., Sample C.A., Setou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Vitarolo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilmink L.G., Wymshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
 RA Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Miyazaki A., Sakai K., Sasaki K., Shibata K., Shingawa A.,  
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573 (2002).  
 RW [3]  
 RP SEQUENCE FROM N.A. (ISOFORM LMW).  
 RC TISSUE=Liver;  
 RX MEDLINE=22388237; PubMed=12477932;  
 RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,  
 RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,  
 RA Bonak S.A., McSway P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,  
 RA Villalon D.K., Muny D.N., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Jansky J., Heiton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green S.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC -1- FUNCTION: (1) Kininogens are inhibitors of thiol proteases; (2)  
 CC HMW-kininogen plays an important role in blood coagulation by  
 CC helping to position optimally prekallikrein and factor XI next to  
 CC factor XII; (3) HMW-kininogen inhibits the thrombin and plasmin-  
 CC induced aggregation of thrombocytes; (4) the active peptide  
 CC bradykinin that is released from HMW-kininogen shows a variety of  
 CC physiological effects: (4A) influence in smooth muscle  
 CC contraction, (4B) induction of hypotension, (4C) natriuresis and  
 CC diuresis, (4D) decrease in blood glucose level, (4E) it is a  
 CC mediator of inflammation and causes (4E1) increase in vascular  
 CC permeability, (4E2) stimulation of nociceptors (4E3) release of  
 CC other mediators of inflammation (e.g. prostaglandins), (4F) it has  
 CC a cardioprotective effect (directly via bradykinin action),  
 CC indirectly via endothelium-derived relaxing factor action; (5)  
 CC LMW-kininogen inhibits the aggregation of thrombocytes; (6) LMW-  
 CC kininogen is in contrast to HMW-kininogen not involved in blood  
 CC clotting (by similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- ALTERNATIVE PRODUCTS:  
 CC Name=HMW;  
 CC IsoId=O08677-1; Sequence=Displayed;  
 CC Name=LMW;  
 CC IsoId=O08677-2; Sequence=VSP\_001263; VSP\_001264;  
 CC -1- TISSUE SPECIFICITY: Plasma.  
 CC -1- PTM: Bradykinin is released from kininogen by plasma kallikrein.  
 CC -1- SIMILARITY: Contains 3 cysteine-like domains.  
 CC -----  
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way







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DR EMBL, M11884; AAA41487.1; ..
DR EMBL, M14369; AAA41484.1; ..
DR EMBL, M14369; AAA41485.1; ALT_SEQ.
DR EMBL, M16455; AAA41482.1; ..
DR PIR; A25486; A25486.
DR PIR; A28055; A28055.
DR InterPro; IPR000010; Cystatin.
DR InterPro; IPR002395; Kininogen.
DR Pfam; PF00031; cystatin; 3.
DR PRINTS; PR00334; KININOGEN.
DR SMART; SM00043; CY; 3.
DR PROSITE; PS00287; CYSTATIN; 2.
KW Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
KW Bradykinin; Blood coagulation; Inflammatory response; Signal,
KW Alternative splicing; Multigene family.
FT SIGNAL 1 18
FT CHAIN 19 639
FT CHAIN 19 380 KININOGEN.
FT PEPTIDE 381 389 KININOGEN HEAVY CHAIN.
FT CHAIN 390 639 BRADYKININ.
FT CHAIN 390 639 KININOGEN LIGHT CHAIN.
FT DOMAIN 19 136 CYSTATIN-LIKE 1.
FT DOMAIN 137 258 CYSTATIN-LIKE 2.
FT DOMAIN 259 380 CYSTATIN-LIKE 3.
FT DOMAIN 439 514 HIS-RICH.
FT DOMAIN 514 609 INTERCHAIN (BY SIMILARITY).
FT DISULFID 28 609
FT DISULFID 83 94 BY SIMILARITY.
FT DISULFID 107 126 BY SIMILARITY.
FT DISULFID 142 145 BY SIMILARITY.
FT DISULFID 206 218 BY SIMILARITY.
FT DISULFID 229 248 BY SIMILARITY.
FT DISULFID 264 267 BY SIMILARITY.
FT DISULFID 328 340 BY SIMILARITY.
FT DISULFID 351 370 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 127 127 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 529 529 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 529 529 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 402 433 VSPSVIARVORERDPGNEQPIHGHGMLHAKO -> RLNS
FT FT CEYKGRLLKAGAPAPERQAEASTVTP (in isoform
FT FT LAM)
FT FT /FTid-vsp 001265.
FT FT Missing (in isoform LAM).
FT FT /FTid-vsp 001266.
FT FT E -> K (in REF. 2).
FT FT
FT VARSPLIC 434 639
FT CONFLICT 61 61
FT SEQUENCE 639 AA; 70933 MW; D3172DF94FF56AF5 CRC64;
Query Match 59.7%; Score 410; DB 1; Length 639;
Best Local Similarity 66.4%; Pred. NO. 2e-31;
Matches 77; Conservative 13; Mismatches 26; Indels 0; Gaps 0;
OY 3 GKDPVPTKICVCPDRPTNSPELESTLTHITKLNAENATFVKIDNVKAROVV 62
DB 253 GDLFLPDLPCPCPRNPVPSPELKEALGSLAQLAENNTFFFKIDTVKATSVV 312
OY 63 AGKXYPDFVARETTCKESNEELTESCTKLGSLDCAEVVVVPEKKIYPTV 118
DB 313 AGTKVIEPIARETKCKEENAEALTADCTKRLGSLNCNANVYRPNKVVPTV 368
RESULT 8
ID KNT2_RAT
AC P08932;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE T-kininogen II precursor (Major acute phase protein) (Alpha-1-MAP)
DE (Thioctatin) (Contains: T-kinin).
OS Rattus norvegicus (Rat).
OC Mammalia; Euteleostomi; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Sakaryota; Metazoa; Chordata; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86008264; PubMed=2413018;
RA Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.;
RT "Primary structures of the mRNAs encoding the rat precursors for
RT bradykinin and T-kinin. Structural relationship of kininogens with
RT major acute phase protein and alpha 1-cysteine proteinase
RT inhibitor."
RL J. Biol. Chem. 260:12054-12059(1985).
CC -!- FUNCTION: Kininogens are plasma glycoproteins with a number of
CC functions: (1) as precursor of the active peptide bradykinin they
CC effect smooth muscle contraction, induction of hypotension and
CC increase of vascular permeability. (2) They play a role in blood
CC coagulation by helping to position optimally prekallikrein and
CC factor XI next to factor XII. (3) They are inhibitor of thiol
CC proteases.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Plasma.
CC -!- INDUCTION: In response to an inflammatory stimulant. T-kininogen
CC II synthesis is induced and the plasma concentration of
CC T-kininogen I is raised.
CC -!- PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT
CC IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA
CC KALLIKREIN.
CC -!- MISCELLANEOUS: Rats express four types of kininogens, the
CC classical HMW and LMW kininogens produced by alternative splicing
CC of the same gene, and two additional LMW-like kininogens: T-I and
CC T-II.
CC -!- SIMILARITY: Contains 3 cystatin-like domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC EMBL; M11885; AAA41491.1; ..
CC PIR; B28055; B28055.
CC GlycoSuiteDB; G08932; ..
CC InterPro; IPR000010; Cystatin.
CC Pfam; PF00031; cystatin; 3.
CC SMART; SM00043; CY; 3.
CC PROSITE; PS00287; CYSTATIN; 2.
KW Glycoprotein; Plasma; Repeat; Vasodilator; Multigene family;
KW Thiol protease inhibitor; Bradykinin; Acute phase; Signal.
FT SIGNAL 1 18
FT CHAIN 19 430 KININOGEN, T-II.
FT CHAIN 19 375 HEAVY CHAIN.
FT PEPTIDE 376 386 T-KININ.
FT CHAIN 387 430 LIGHT CHAIN.
FT DOMAIN 19 135 CYSTATIN-LIKE 1.
FT DOMAIN 136 257 CYSTATIN-LIKE 2.
FT DOMAIN 258 375 CYSTATIN-LIKE 3.
FT DISULFID 28 404 INTERCHAIN (BY SIMILARITY).
FT DISULFID 83 94 BY SIMILARITY.
FT DISULFID 107 125 BY SIMILARITY.
FT DISULFID 141 144 BY SIMILARITY.
FT DISULFID 205 217 BY SIMILARITY.
FT DISULFID 228 247 BY SIMILARITY.
FT DISULFID 263 266 BY SIMILARITY.
FT DISULFID 327 339 BY SIMILARITY.
FT DISULFID 350 369 BY SIMILARITY.
FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 126 126 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 168 168 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 204 204 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 326 326 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 430 AA; 43524 MW; 43EDF02D1BF55076 CRC64;
Query Match 56.5%; Score 388; DB 1; Length 430;

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Best Local Similarity 62.1%, Pred. No. 1.6e-29, Matches 72; Conservative 15; Mismatches 29; Indels 0; Gaps 0;

QY 3 GNDVPQPTKICVGCPRDIPNTSPLESETLTHITKLNAENATPYFKIDNVKARQVYV 62  
DB 252 GDDLFLSLPKKCFGCPKQNPVDSPELKEALGHSIAQLNAQHNLFPFKIDTVKATQGV 311  
QY 63 AGKKYFDFVARETTCSENEELTESCETKGLQSLDCNAEYVVPWPKKIYPTV 118  
DB 312 AGTKYVIEFARETNCKQNTVELTADCTEYKGLQSLNCNANVYRPNWPKVPTV 367

RESULT 9

QY KNTL RAT STANDARD; PRT; 430 AA.

DB KNTL RAT STANDARD; PRT; 430 AA.

QY 01-NOV-1996 (Rel. 03, Created)  
DB 01-NOV-1998 (Rel. 09, Last sequence update)  
QY 15-MAR-2004 (Rel. 43, Last annotation update)  
DB 15-MAR-2004 (Rel. 43, Last annotation update)  
QY T-kininogen I precursor (Major acute phase protein) (Alpha-1-MAP)  
DB T-kininogen I precursor (Major acute phase protein) (Alpha-1-MAP)  
QY (Thioestatin) [Contains: T-kinin]  
DB (Thioestatin) [Contains: T-kinin]  
QY Rattus norvegicus (Rat)  
DB Rattus norvegicus (Rat)  
QY Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
DB Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
QY Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
DB Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
QY NCBI\_TaxID:10116;  
DB NCBI\_TaxID:10116;  
QY SEQUENCE FROM N.A.  
DB SEQUENCE FROM N.A.  
QY MEDLINE=86009264; PubMed=24113018;  
DB MEDLINE=86009264; PubMed=24113018;  
QY Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.,  
DB Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.,  
QY "Primary structures of the mRNAs encoding the rat precursors for  
DB "Primary structures of the mRNAs encoding the rat precursors for  
QY bradykinin and T-kinin. Structural relationship of kininogens with  
DB bradykinin and T-kinin. Structural relationship of kininogens with  
QY major acute phase protein and alpha 1-cysteine proteinase  
DB major acute phase protein and alpha 1-cysteine proteinase  
QY inhibitor.",  
DB inhibitor.",  
QY J. Biol. Chem. 260:12054-12059 (1985).  
DB J. Biol. Chem. 260:12054-12059 (1985).  
QY [2]  
DB [2]  
QY SEQUENCE OF 5-430 FROM N.A., AND PARTIAL SEQUENCE.  
DB SEQUENCE OF 5-430 FROM N.A., AND PARTIAL SEQUENCE.  
QY MEDLINE=86008266; PubMed=2413019;  
DB MEDLINE=86008266; PubMed=2413019;  
QY Anderson K.P., Heath E.C.,  
DB Anderson K.P., Heath E.C.,  
QY "The relationship between rat major acute phase protein and the  
DB "The relationship between rat major acute phase protein and the  
QY kininogens.",  
DB kininogens.",  
QY J. Biol. Chem. 260:12065-12071 (1985).  
DB J. Biol. Chem. 260:12065-12071 (1985).  
QY [3]  
DB [3]  
QY SEQUENCE OF 7-430 FROM N.A.  
DB SEQUENCE OF 7-430 FROM N.A.  
QY MEDLINE=8127563; PubMed=2578992;  
DB MEDLINE=8127563; PubMed=2578992;  
QY Cole I., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.,  
DB Cole I., Inglis A.S., Roxburgh C.M., Howlett G.J., Schreiber G.,  
QY "Major acute phase alpha 1-protein of the rat is homologous to bovine  
DB "Major acute phase alpha 1-protein of the rat is homologous to bovine  
QY kininogen and contains the sequence for bradykinin: its synthesis is  
DB kininogen and contains the sequence for bradykinin: its synthesis is  
QY regulated at the mRNA level.",  
DB regulated at the mRNA level.",  
QY FEBS Lett. 182:57-61 (1985).  
DB FEBS Lett. 182:57-61 (1985).  
QY [4]  
DB [4]  
QY SEQUENCE OF 1-65 FROM N.A.  
DB SEQUENCE OF 1-65 FROM N.A.  
QY MEDLINE=87250580; PubMed=2439509;  
DB MEDLINE=87250580; PubMed=2439509;  
QY Fung W.-P., Schreiber G.,  
DB Fung W.-P., Schreiber G.,  
QY "Structure and expression of the genes for major acute phase alpha 1-  
DB "Structure and expression of the genes for major acute phase alpha 1-  
QY protein (thioestatin) and kininogen in the rat.",  
DB protein (thioestatin) and kininogen in the rat.",  
QY J. Biol. Chem. 262:9298-9308 (1987).  
DB J. Biol. Chem. 262:9298-9308 (1987).  
QY -1- FUNCTION: Kininogens are plasma glycoproteins with a number of  
DB -1- FUNCTION: Kininogens are plasma glycoproteins with a number of  
QY functions: (1) as precursor of the active peptide bradykinin they  
DB functions: (1) as precursor of the active peptide bradykinin they  
QY effect smooth muscle contraction, induction of hypertension and  
DB effect smooth muscle contraction, induction of hypertension and  
QY increase of vascular permeability. (2) They play a role in blood  
DB increase of vascular permeability. (2) They play a role in blood  
QY coagulation by helping to position optimally prekallikrein and  
DB coagulation by helping to position optimally prekallikrein and  
QY factor XI next to factor XII. (3) They are inhibitor of thiol  
DB factor XI next to factor XII. (3) They are inhibitor of thiol  
QY proteases.  
DB proteases.  
QY -1- SUBCELLULAR LOCATION: Extracellular.  
DB -1- SUBCELLULAR LOCATION: Extracellular.  
QY -1- TISSUE SPECIFICITY: Plasma.  
DB -1- TISSUE SPECIFICITY: Plasma.  
QY -1- INDUCTION: In response to an inflammatory stimulant. T-kininogen  
DB -1- INDUCTION: In response to an inflammatory stimulant. T-kininogen  
QY II synthesis is induced and the plasma concentration of  
DB II synthesis is induced and the plasma concentration of  
QY T-kininogen I is raised.  
DB T-kininogen I is raised.  
QY -1- PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT  
DB -1- PTM: AS T-KININ IS PRECEDED BY A MET INSTEAD OF AN ARG OR LYS, IT  
QY IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA  
DB IS NOT RELEASED FROM ITS PRECURSOR BY EITHER TISSUE OR PLASMA  
QY KALLIKREIN.  
DB KALLIKREIN.  
QY -1- MISCELLANEOUS: Rata express four types of kininogens: the  
DB -1- MISCELLANEOUS: Rata express four types of kininogens: the

CC Classical HW and LMW kininogens produced by alternative splicing  
CC of the same gene, and two additional LMW-like kininogens, T-I and  
CC T-II.  
CC  
CC -1- SIMILARITY: Contains 3 cystatin-like domains.  
CC  
CC -1- CAUTION: In addition to the conflicts described in the feature  
CC table, Ref.2 sequence differs from that shown in positions 257,  
CC 262, 268, 269, 295, 314, 331, 332 and 389. In all these  
CC positions the alternate amino acid is the one present in T-II  
CC kininogen.  
CC  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; M11803; AAA41489.1; -  
CC EMBL; M11861; AAA41370.1; -  
CC EMBL; M16454; AAA41368.1; -  
CC EMBL; X02239; CAA26162.1; ALT\_SEQ.  
CC  
CC PIR; A01286; MGR111.  
CC PIR; A23897; A23897.  
CC PIR; A27115; A27115.  
CC GlycoSuiteDB; P01048; -  
CC InterPro; IPR000010; Cystatin.  
CC Pfam; PF00031; cystatin; 3.  
CC SMART; SM00043; CV; 3.  
CC PROSITE; PS00287; Cystatin; 2.  
CC Glycoprotein; Plasma; Repeat; Vasodilator; Multigene family;  
CC Thiol protease inhibitor; Bradykinin; Acute phase; Signal.  
CC  
CC SIGNAL 1 18  
CC CHAIN 1 430 KININOGEN, T-I.  
CC CHAIN 19 375 HEAVY CHAIN.  
CC CHAIN 376 386 T-KININ.  
CC CHAIN 387 430 LIGHT CHAIN.  
CC DOMAIN 19 135 CYSTATIN-LIKE 1.  
CC DOMAIN 136 257 CYSTATIN-LIKE 2.  
CC DOMAIN 258 375 CYSTATIN-LIKE 3.  
CC DISULFID 28 404 INTERCHAIN (BY SIMILARITY).  
CC DISULFID 83 94 BY SIMILARITY.  
CC DISULFID 107 125 BY SIMILARITY.  
CC DISULFID 141 144 BY SIMILARITY.  
CC DISULFID 205 217 BY SIMILARITY.  
CC DISULFID 228 247 BY SIMILARITY.  
CC DISULFID 263 266 BY SIMILARITY.  
CC DISULFID 327 339 BY SIMILARITY.  
CC DISULFID 350 369 BY SIMILARITY.  
CC CARBOHYD 82 92 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC CARBOHYD 126 126 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC CARBOHYD 168 168 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC CARBOHYD 204 204 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC CARBOHYD 326 336 N-LINKED (GLCNAC... ) (POTENTIAL).  
CC CONFLICT 26 28 LNC -> MDR (IN REF. 2).  
CC CONFLICT 55 55 V -> L (IN REF. 2).  
CC CONFLICT 61 61 E -> K (IN REF. 1).  
CC CONFLICT 83 83 C -> Y (IN REF. 1).  
CC CONFLICT 166 166 S -> F (IN REF. 2 AND 3).  
CC CONFLICT 179 181 REV -> TKI (IN REF. 2).  
CC CONFLICT 193 193 N -> D (IN REF. 2).  
CC CONFLICT 212 212 S -> F (IN REF. 2).  
CC CONFLICT 214 214 T -> R (IN REF. 3).  
CC CONFLICT 229 229 R -> Y (IN REF. 2).  
CC CONFLICT 233 231 E -> S (IN REF. 2).  
CC CONFLICT 257 257 R -> K (IN REF. 2).  
CC CONFLICT 262 262 R -> F (IN REF. 2).  
CC CONFLICT 264 264 RE -> QN (IN REF. 2).  
CC CONFLICT 268 269 I -> L (IN REF. 2).  
CC CONFLICT 295 295 VI -> TK (IN REF. 2).  
CC CONFLICT 314 315 SK -> TN (IN REF. 2).  
CC CONFLICT 331 332 R -> O (IN REF. 2).  
CC CONFLICT 389 389

PT CONFLICT 414 414 R -> G (IN REF. 2 AND 3).  
PT CONFLICT 415 415 A -> L (IN REF. 2).  
PT CONFLICT 420 421 DH -> ER (IN REF. 3).  
PT CONFLICT 430 430 P -> S (IN REF. 1).  
SQ SEQUENCE 430 AA, 47715 MW, PAEBB787AF4723C3 CRC64;

Query Match 55.3%, Score 380, DB 1, Length 430;  
Best Local Similarity 62.1%, Pred No. 98-29, 30, Indels 0, Gaps 0;  
Matches 72, Conservative 14, Mismatches 30, Indels 0, Gaps 0;

QY 3 GDFVQPTKICVGCPRDIPNPSLEETLTHITKLAENNAATPYFKINVKARVQV 62  
DB 252 GDFVQPTKICVGCPRDIPNPSLEETLTHITKLAENNAATPYFKINVKARVQV 62

QY 63 AGKYPIDFVARETTCSEKSNBELTESCE--TKKLGSLDCAEAVVVPWEKKIYFTV 118  
DB 312 AGVIVYIEFIARETNCQSKQKTELTADCTKHLGSLDCAEAVVVPWEKKIYFTV 367

RESULT 10  
ID CYTF MOUSE STANDARD, PRT, 144 AA.  
AC Q89058.  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Cystatin P precursor (Leukocystatin) (Cystatin 7) (Cystatin-like  
DE metastasis-associated protein) (CMAP).  
GN CST7.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98298157, PubMed=9632704;  
RA Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,  
RA Xu Y., Weiss M., Ikeda M., Liggert D., Helms A., Caux C., Lebecque S.,  
RA Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.,  
RA "Leukocystatin, a new class II cystatin expressed selectively by  
RT hematopoietic cells.",  
RL J. Biol. Chem. 273:16400-16408(1998).  
CC -!- FUNCTION: Inhibits pepsin and cathepsin L but with affinities  
CC lower than other cystatins. May play a role in immune regulation  
CC through inhibition of a unique target in the hematopoietic system.  
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).  
CC -!- SIMILARITY: Belongs to the cystatin family.  
CC -----  
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CC or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC -----  
DR EMBL; AF031826; AAC40140.1; --  
DR EMBL; AF031825; AAC40139.1; --  
DR HSPG; P01034; IG96.  
DR MGD; MGI:1298217; Cst7.  
DR InterPro; IPR000010; Cystatin.  
DR Pfam; PF00031; cystatin; 1.  
DR SMART; SM00043; Cst\_1.  
DR PROSITE; PS00287; CYSTATIN; FALSE NEG.  
KW Thiol protease inhibitor; Glycoprotein; Signal.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 144 CYSTATIN P.  
FT ACT\_SITE 36 36 REACTIVE SITE.  
FT SITE 80 84 SECONDARY AREA OF CONTACT.  
FT DISULFID 98 109 BY SIMILARITY.  
FT DISULFID 123 143 BY SIMILARITY.  
SQ SEQUENCE 144 AA, 16380 MW, B5837334C1B4A89C CRC64;

Query Match 25.0%, Score 171.5, DB 1, Length 144;  
Best Local Similarity 35.5%, Pred No. 1.7e-09;  
Matches 39, Conservative 22, Mismatches 42, Indels 7, Gaps 3;

QY 4 KDFVQPTKICVGCPRDIPNPSLEETLTHITKLAENNAATPYFKINVKARVQV 63  
DB 27 KDLI---SSVKGPFPTTETNNPGVLAARHSVEKNNCTNDIPLFKSHVSKALVQV 83

QY 64 GKYPIDFVARETTCSEKSNBELTESCE--TKKLGSLDCAEAVVVPW 110  
DB 84 GLKYPLEVYIGRTTCKTMRHQL-DNCDFTNPALAKETLYCYSEVVVPM 132

RESULT 11  
ID CYTF HUMAN STANDARD, PRT, 145 AA.  
AC Q76056, Q9UED4.  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Cystatin P precursor (Leukocystatin) (Cystatin 7) (Cystatin-like  
DE metastasis-associated protein) (CMAP).  
GN CST7.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98406131, PubMed=9733783;  
RA Ni J., Fernandez M.A., Danielsson L., Chillakuru R.A., Zhang J.,  
RA Grubb A., Su J., Gentz R., Abrahamson M.,  
RA "Cystatin P is a glycosylated human low molecular weight cysteine  
RT proteinase inhibitor.",  
RL J. Biol. Chem. 273:24797-24804(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98298157, PubMed=9632704;  
RA Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,  
RA Xu Y., Weiss M., Ikeda M., Liggert D., Helms A., Caux C., Lebecque S.,  
RA Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.,  
RA "Leukocystatin, a new class II cystatin expressed selectively by  
RT hematopoietic cells.",  
RL J. Biol. Chem. 273:16400-16408(1998).  
RN [3]  
RP SEQUENCE FROM N.A.  
RA Morita M., Arakawa H., Yoshiuchi N.;  
RT "Human homologue of murine CMAP.",  
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20399571, PubMed=10945474;  
RA Morita M., Hara Y., Tanai Y., Arakawa H., Nishimura S.,  
RT "Genomic construct and mapping of the gene for CMAP  
RT (Leukocystatin/Cystatin P, CST7) and identification of a proximal  
RT novel gene, BSCV (C20orf3).",  
RL Genomics 67:87-91(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21639749, PubMed=11780052;  
RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Baguley C.L.,  
RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,  
RA Beasley O.P., Bird C.P., Blakey S.B., Bridgman A.M., Brown A.J.,  
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,  
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
RA Clegg S., Cobley V.B., Collier R.E., Connor R.B., Corby N.R.,  
RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,  
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
RA Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,  
RA Hammond S., Harley J.B., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
RA Huckle E., Hunt A.R., Hunt S.E., Jackson K., Johnson C.M., Johnson D.,  
RA Kay M.P., Kimberley A.M., King A., Knightes A., Laird G.K., Lawlor S.,



QY 8 OPTKICVCGPRDIPNTPSELESLTHITKLNENATFYFKIDNVKQVQVAGKY 67  
 Db 31 KPFR--LVGPMDSVZEEGRVAFSEVETKNSNDMTHSRALQVVRKQIVAGVNY 88  
 QY 68 FIDFVARITTCGSKESNELTESC---ETTKLGOSLDCAEVVVPWKKIYPTVTWNHWE 124  
 Db 89 FLVDELGRTTCTK--TOPNLDNCPFHEOPHLKAKFPCFOIYTVFQO----GWTLSKST 142  
 QY 125 CE 126  
 Db 143 CQ 144

RESULT 13  
 CYTM\_HUMAN  
 ID CYTM\_HUMAN STANDARD; PRT; 149 AA.  
 AC Q15828;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Cystatin M precursor (Cystatin E).  
 GN C8T6.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 CC NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97150844; PubMed=8995380;  
 RA Sotiropoulos G., Anisowicz A., Sager R.;  
 RA "Identification, cloning, and characterization of cystatin M, a novel  
 RT cysteine proteinase inhibitor, down-regulated in breast cancer.";  
 RL J. Biol. Chem. 272:903-910(1997).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97256812; PubMed=9099741;  
 RA Ni J., Abrahamson M., Zhang M., Fernandez M.A., Grubb A., Su J.,  
 RA Yu G.L., Li Y., Parmelee D., Xing L., Coleman T.A., Gentz S.,  
 RA Thakura R., Nguyen N., Hesselberg M., Gentz R.;  
 RT "Cystatin E is a novel human cysteine proteinase inhibitor with  
 RT structural resemblance to family 2 cystatins.";  
 RL J. Biol. Chem. 272:10853-10858(1997).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Prostate;  
 RX MEDLINE=2238257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins P.S., Wagner L., Shenman C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Rabe S.S., Lochell N.A., Peters G.J., Abramson R.D., Mullen S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN (4)  
 RP CHARACTERIZATION, AND TISSUE SPECIFICITY.  
 RX MEDLINE=21246880; PubMed=11148457;  
 RA Zeewen P.L., Van Vlijmen-Willems I.M., Jansen B.J., Sotiropoulos G.,  
 RA Carls J.H., Mels J.F., Jansen J.J., Van Kuilen P., Schalkwijk J.;  
 RT "Cystatin M/E expression is restricted to differentiated epidermal  
 RT keratinocytes and sweat glands: a new skin-specific proteinase

RT inhibitor that is a target for cross-linking by transglutaminase.";  
 RL J. Invest. Dermatol. 116:693-701(2001).  
 CC - FUNCTION: Shows moderate inhibition of cathepsin B but is not  
 CC active against cathepsin C.  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - TISSUE SPECIFICITY: Restricted to the stratum granulosum of normal  
 CC skin, the stratum granulosum/epinosum of psoriatic skin, and the  
 CC secretory coils of eccrine sweat glands. Low expression levels are  
 CC found in the nasal cavity.  
 CC - PFM: Substrate for transglutaminases. Acts as an acyl acceptor but  
 CC not as an acyl donor.  
 CC - SIMILARITY: Belongs to the cystatin family.  
 CC  
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 CC  
 CC EMBL; U62800; RAB06566.1; -  
 CC EMBL; U81233; RAB51305.1; -  
 CC EMBL; BC011334; AAH1334.1; -  
 CC HSRP; P01038; ICEW.  
 CC Gene; HGNC:2478; CST6.  
 CC MIM; 601891; -  
 CC GO; GO:0004869; F:cysteine protease inhibitor activity; TAS.  
 CC GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.  
 CC InterPro; IPR000010; Cystatin.  
 CC Pfam; PF00031; cystatin; 1.  
 CC SMART; SM00043; CV; 1.  
 CC PROSITE; PS00287; CYSTATIN; 1.  
 CC K101 protease inhibitor; Signal, Glycoprotein.  
 FT SIGNAL 1 28  
 FT CHAIN 1 149  
 FT ACT SITE 26 36  
 FT SITE 86 84  
 FT DISULFID 98 113  
 FT DISULFID 126 146  
 FT CARBOHYD 137 137  
 SQ SEQUENCE 149 AA; 16511 MW; 2076A78BFC9FAC8C CRC64;  
 Query Match 20.2%; Score 136.5; DB 1; Length 149;  
 Best Local Similarity 31.5%; Pred. No. 2.4e-06;  
 Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;  
 QY 10 PTKICVCGPRDIPNTPSELESLTHITKLNENATFYFKIDNVKQVQVAGKYFI 69  
 Db 30 PQRVWGLRDLSPDDQVQKAAQAVSYNGMSITFRDTHIIKQSLVAGIKYFL 89  
 QY 70 DFVARETTCSE-----SNEELTESCTYKLGQ--SLDCNAEVVVPWE 111  
 Db 90 TREMGSTDCRTRVTDGVLT-TCPLAAGAQCKLRCDFVLVVPQ 136

RESULT 14  
 CYTC\_BOVIN  
 ID CYTC\_BOVIN STANDARD; PRT; 148 AA.  
 AC P01035;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 15-JUL-1999 (Rel. 35, Last sequence update)  
 DT 28-FEB-2003 (Rel. 43, Last annotation update)  
 DE Cystatin C precursor (Colostrum thiol proteinase inhibitor).  
 GN C8T3.  
 OS Bos taurus (Bovine).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 CC Bovidae; Bovinae; Bos.  
 CC NCBI\_TaxID=9913;  
 RN (1)  
 RP SEQUENCE FROM N.A.; SEQUENCE OF 66-83, AND CHARACTERIZATION.  
 RT TISSUE=Cerebrospinal fluid, and Choroid plexus;

RX MEDLINE=98094199; PubMed=9434110;  
 RA Olson S.-L., Ek B., Wilm M., Broberg S., Raak L., Bjork I.,  
 RI "Molecular cloning and N-terminal analysis of bovine cystatin C  
 RT identification of a full-length N-terminal region."  
 RL Biochim. Biophys. Acta 1343:203-210(1997).  
 RN [2]  
 RP SEQUENCE OF 37-148.  
 RX MEDLINE=85311205; PubMed=3991407;  
 RA Hirado M., Tsunawake S., Sakiyama F., Minobe M., Fujii S.,  
 RI "Complete amino acid sequence of bovine colostrum low-Mr cysteine  
 RT proteinase inhibitor."  
 RL FEBS Lett. 186:41-45(1985).  
 RN [1]  
 RP FUNCTION: This is a thiol proteinase inhibitor.  
 RX MASS SPECTROMETRY; MW=13420; METHOD=MALDI.  
 CC -1- SIMILARITY: Belongs to the cystatin family.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; Y10811; CAA71771.1; .  
 DR HSP; P01034; I96.  
 DR InterPro; IPR000010; Cystatin.  
 DR Pfam; PF00031; cystatin; 1.  
 DR SMART; SM00043; CY; 1.  
 DR PROSITE; PS00287; CYSTATIN; 1.  
 KM Thiol protease inhibitor; signal; Pyroglutamate carboxylic acid.  
 FT SIGNAL 1 30  
 FT CHAIN 31 148  
 FT MOD\_RES 31 31 PYROGLUTAMATE CARBOXYLIC ACID (PROBABLE).  
 FT ACT\_SITE 40 40 REACTIVE SITE.  
 FT SITE 84 88 SECONDARY AREA OF CONTACT.  
 FT DISULFID 102 112 BY SIMILARITY.  
 FT DISULFID 126 146 BY SIMILARITY.  
 SQ SEQUENCE 148 AA; 16265 MW; BE740FE37CEB9FOE CRC64;  
 Query Match 20.0%; Score 137.5; DB 1; Length 148;  
 Best Local Similarity 28.8%; Pred. No. 3e-06;  
 Matches 32; Conservative 25; Mismatches 35; Indels 19; Gaps 4;  
 Oy 24 NSPELEETLTHITKLNENATFYKIDNVKARVGVAGKYPIDFVARETTCSESN 83  
 Db 48 NEEGVQELSFVASENFKNSDVAQSVRVVRVARKQVGMGYFLDVELGRTCTK--S 105  
 Oy 84 EELTSC-----STKGLQSLDCNAEVVYVPEKKIYPTVVARHCE 126  
 Db 106 QANLDCPPHNPQHLKREK-----CSFQVYVPEWNN-----TINLVKESQ 147  
 RESULT 15  
 ID\_PETB RAT STANDARD; PRT; 378 AA.  
 AC Q90X79;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Fetuin-B precursor (IRL685).  
 GN FETUB.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
 RX MEDLINE=20407138; PubMed=10347975;  
 RA Olivier E., Soury E., Ruminy P., Rouson A., Parmentier P., Davenau M.,  
 RA Saller J.-P.,  
 RT "Fetuin-B, a second member of the fetuin family in mammals."  
 RN [1]

RL Biochem. J. 350:589-597(2000).  
 CC -1- SUBCELLULAR LOCATION: Secreted (Potential).  
 CC -1- TISSUE SPECIFICITY: Liver.  
 CC -1- SIMILARITY: Belongs to the fetuin family.  
 CC -1- SIMILARITY: Contains 2 cystatin-like domains.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; AJ242926; CAB62543.1; .  
 DR InterPro; IPR000010; Cystatin.  
 DR Pfam; PF00031; cystatin; 2.  
 DR SMART; SM00043; CY; 2.  
 DR PROSITE; PS01254; FETUIN\_1; 1.  
 DR PROSITE; PS01255; FETUIN\_2; 1.  
 KM Glycoprotein; signal; Repeat.  
 FT SIGNAL 1 18  
 FT CHAIN 19 378  
 FT DOMAIN 27 152  
 FT DOMAIN 153 273  
 FT DISULFID 96 107  
 FT DISULFID 120 140  
 FT DISULFID 154 157  
 FT DISULFID 217 224  
 FT DISULFID 237 260  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC...) (POTENTIAL).  
 FT CARBOHYD 139 139 N-LINKED (GLCNAC...) (POTENTIAL).  
 SQ SEQUENCE 378 AA; 41532 MW; 066C0A5C3B03C878 CRC64;  
 Query Match 19.7%; Score 135; DB 1; Length 378;  
 Best Local Similarity 25.8%; Pred. No. 1.5e-05;  
 Matches 33; Conservative 32; Mismatches 49; Indels 14; Gaps 5;  
 Oy 7 VQPPTK-----ICVGCPRDPTNSPLEETLTHITKLNENATFYKIDNVKARVQV 61  
 Db 142 LRPVSKRKIHSMCPDCPHVDLSPVLEAATSLAKPNSNPMSQYALV-KVTKATQW 200  
 Oy 62 VAGKYPIDFVARETTCSESNELTESCTKGLQSLDCNAEVVYVPEW--EKIYPTV 119  
 Db 201 VVGPSYFVEYLKESPTQSDSCSLQASDSEPVGL---CGSLKSPGVPPQPKKTVT 257  
 Oy 120 VNHWECEP 127  
 Db 258 VS---CEP 262  
 Search completed: September 24, 2004, 14:09:13  
 Job time : 9.636 secs



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OM protein - protein search, using sw model

Run on: September 24, 2004, 14:06:08, Search time 13.716 Seconds  
(without alignment)  
890.662 Million cell updates/sec

Title: US-10-661-784-3

Perfect score: 687

Sequence: 1 GSGKDFVQPTKICVGRD.....VPMKKYKTYTVNHWCEEF 127

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: PIR 78:  
1: PIR1:  
2: PIR2:  
3: PIR3:  
4: PIR4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | ID       | Description           |
|------------|-------|-------------|--------|----------|-----------------------|
| 1          | 618   | 90.0        | 427    | 1 KGHUL1 | kininogen, LHM pre    |
| 2          | 618   | 90.0        | 444    | 1 KGHUH1 | kininogen, LHM pre    |
| 3          | 440   | 64.0        | 436    | 1 KGBOL1 | kininogen, LHM I p    |
| 4          | 440   | 64.0        | 621    | 1 KGBOL1 | kininogen, LHM I p    |
| 5          | 413   | 60.1        | 434    | 1 KGBOL2 | kininogen, LHM I p    |
| 6          | 413   | 60.1        | 619    | 1 KGBOL2 | kininogen, LHM I p    |
| 7          | 410   | 59.7        | 433    | 2 A28055 | K-kininogen, LHM I    |
| 8          | 410   | 59.7        | 639    | 2 A28055 | K-kininogen, LHM I p  |
| 9          | 388   | 56.5        | 430    | 2 A23897 | major acute phase     |
| 10         | 388   | 56.5        | 430    | 2 B28055 | T-kininogen, LHM I    |
| 11         | 381   | 55.5        | 423    | 1 KGRTM  | major acute phase     |
| 12         | 380   | 55.3        | 430    | 1 KGRTM  | T-kininogen I prec    |
| 13         | 137.5 | 20.0        | 142    | 1 UDRO   | cystatin - bovine     |
| 14         | 132.5 | 19.3        | 146    | 1 UDRO   | cystatin C precursor  |
| 15         | 130   | 18.9        | 127    | 2 S07085 | cystatin C - rat      |
| 16         | 129   | 18.8        | 120    | 2 S10587 | cystatin C - puff ad  |
| 17         | 128   | 18.6        | 111    | 2 A28793 | cystatin C precursor  |
| 18         | 127.5 | 18.6        | 140    | 2 A36163 | cystatin SA precursor |
| 19         | 124.5 | 18.1        | 141    | 2 B29632 | cystatin S precursor  |
| 20         | 118.5 | 17.2        | 139    | 1 UDCH   | cystatin S precursor  |
| 21         | 113   | 16.4        | 141    | 2 JQ1470 | T-kininogen (clone)   |
| 22         | 112   | 16.3        | 91     | 2 S68035 | cystatin - chum sa    |
| 23         | 112   | 16.3        | 91     | 2 S68035 | cystatin SN precursor |
| 24         | 111   | 16.2        | 111    | 1 JC2040 | cystatin S precursor  |
| 25         | 109.5 | 15.9        | 141    | 1 UDHUP2 | hypothetical prote    |
| 26         | 108.5 | 15.8        | 141    | 1 UDHUP1 | cystatin precursor    |
| 27         | 107   | 15.6        | 139    | 2 T33740 | chondrocyte           |
| 28         | 106   | 15.4        | 132    | 2 JC4918 | chondrocyte           |
| 29         | 105.5 | 15.4        | 162    | 2 A43428 | chondrocyte           |

## RESULT 1

KGHUL1  
kininogen, LHM precursor [validated] - human  
N/Alternate names: alpha-2-thiol proteinase inhibitor; prokininogen  
N/Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen  
C/Species: Homo sapiens (man)  
C/Date: 06-Jul-1982 #sequence-revision 27-Nov-1985 #text-change 08-Dec-2000  
C/Accession: A01280, B25276, A27900, A27699, A31905, A34030  
R/Okubo, I.; Rautsch, K.; Takasawa, T.; Shiohara, M.; Sasaki, M.  
Biochemistry 23, 5691-5697, 1984  
A/Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its iden  
A/Reference number: A90490; MUID:85122621; PMID:6441591  
A/Accession: A01280  
A/Molecule type: mRNA  
A/Residues: 1-427 <OH>  
A/Cross-references: GB:K02566; NID:G177889; PIDN:AAA35497.1; PID:G177890  
R/Takagaki, Y.; Kitamura, N.; Nakanishi, S.  
J. Biol. Chem. 260, 8601-8609, 1985  
A/Title: Cloning and sequence analysis of cDNAs for human high molecular weight and lo  
A/Reference number: A32544; MUID:85234582; PMID:2989293  
A/Accession: B25276  
A/Molecule type: mRNA  
A/Residues: 1-427 <TA>  
A/Cross-references: GB:M11437; NID:G186751; PIDN:AA59551.1; PID:G386853  
R/Lottspeich, F.; Kellermann, J.; Henschen, A.; Rautsch, G.; Mueller-Esterl, W.  
in Kinin IV - part A. Greenbaum, L.M., and Margolius, H.S., eds., pp.91-95, Plenum, Ne  
A/Title: Amino acid sequence of the light chain of human low molecular mass kininogen.  
A/Reference number: A27900  
A/Accession: A27900  
A/Molecule type: protein  
A/Residues: 390-427 <LOT>  
R/Mindrou, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.  
Biochem. Biophys. Res. Commun. 152, 519-526, 1988  
A/Title: A new kinin moiety in human plasma kininogens.  
A/Reference number: A27699; MUID:88209021; PMID:3365237  
A/Accession: A27699  
A/Molecule type: protein  
A/Residues: 380-389 <MIN>  
R/Maeda, H.; Matsumura, Y.; Kato, H.  
J. Biol. Chem. 263, 16051-16054, 1988  
A/Title: Purification and identification of [hydroxyprolyl(3)]-bradykinin in ascitic fl  
A/Reference number: A31905; MUID:89034061; PMID:3182782  
A/Accession: A31905  
A/Molecule type: protein  
A/Residues: 381-389 <MA>  
R/Sasaguri, M.; Ikeda, M.; Idetani, M.; Arakawa, K.  
Biochem. Biophys. Res. Commun. 150, 511-516, 1988  
A/Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human pl  
A/Reference number: A34030; MUID:88106632; PMID:3337729  
A/Accession: A34030  
A/Molecule type: protein  
A/Residues: 380-389 <SAS>

## ALIGNMENTS

|    |       |      |     |   |        |
|----|-------|------|-----|---|--------|
| 30 | 102   | 14.8 | 122 | 2 | A43644 |
| 31 | 101.5 | 14.8 | 123 | 2 | JC4536 |
| 32 | 97.5  | 14.2 | 135 | 2 | JC4007 |
| 33 | 97    | 14.1 | 142 | 2 | A47142 |
| 34 | 95.5  | 13.9 | 143 | 2 | T33301 |
| 35 | 94.5  | 13.8 | 145 | 2 | S21094 |
| 36 | 93.5  | 13.6 | 139 | 2 | A45361 |
| 37 | 92    | 13.4 | 100 | 2 | JH0269 |
| 38 | 91.5  | 13.3 | 135 | 2 | S27239 |
| 39 | 91.5  | 13.3 | 135 | 2 | A32827 |
| 40 | 88.5  | 12.9 | 125 | 2 | T00752 |
| 41 | 88.5  | 12.9 | 134 | 2 | S54828 |
| 42 | 88.5  | 12.9 | 134 | 2 | JC4882 |
| 43 | 88    | 12.8 | 199 | 2 | S65071 |
| 44 | 88    | 12.8 | 367 | 1 | W0HU   |
| 45 | 84.5  | 12.3 | 592 | 2 | T50516 |





A:Experimental source: urine  
A:Note: this peptide had Pro-383 modified to 4-hydroxyproline  
A:Accession: C61495  
A:Molecule type: Protein  
A:Residues: 380-389 <KAT>  
R:Lenaric, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V.  
FEBS Lett. 280, 211-215, 1991  
A:Title: Inactivation of human cystatin C and kininogen by human cathepsin D.  
A:Reference number: S14303, MUID:9119133, PMID:2013314  
A:Accession: S14447  
A:Molecule type: Protein  
A:Residues: 364-359, 'N', 361-375 <LEN2>  
R:Little, S.S.; Johnson, D.A.  
Biochem. J. 307, 341-346, 1995  
A:Title: Human mast cell tryptase isoforms: separation and examination of substrate-specificity  
A:Reference number: S55239, MUID:95251593, PMID:7733667  
A:Accession: S55239  
A:Molecule type: Protein  
A:Residues: 450-452, 'X', 454, 'X', 456 <LIT>  
R:Straczek, J.; Maschi, F.; Le Nguyen, D.; Becchi, M.; Heulin, M.H.; Nebet, P.; Bellevil  
FEBS Lett. 373, 207-211, 1995  
A:Title: Purification from human plasma of a tetrapeptide that potentiates insulin-like  
A:Reference number: S68059, MUID:96033974, PMID:7589467  
A:Accession: S68059  
A:Molecule type: Protein  
A:Residues: 431-434 <GRA>  
R:Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata, T.; Nakanishi, S.  
J. Biol. Chem. 260, 8610-8617, 1985  
A:Title: Structural organization of the human kininogen gene and a model for its evolution  
A:Reference number: A92548, MUID:85234583, PMID:2989394  
A:Contents: annotation; gene organization  
R:Percec, J.V. 52-57, 1968  
Fed. Proc. 27, 52-57, 1968  
A:Title: Structural features of plasma kinins and kininogens.  
A:Reference number: A91455, MUID:90255622, PMID:4952632  
A:Contents: annotation; bradykinin  
C:Comment: The HMW kininogen precursor and the LMW form are produced from the same gene  
C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the  
C:Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is im  
C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i  
xyproline residue is present in the kininogen prior to the release of bradykinin.  
C:Genetics:  
A:Gene: GDB:KNG  
A:Cross-references: GDB:125256; OMIM:228960  
A:Map position: 3q27-3q27  
A:Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3  
C:Superfamily: kininogen; cystatin homology  
C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl  
F:19-644/Product: HMW kininogen I (prokininogen) #status experimental <MATI>  
F:19-379,390-644/Product: HMW kininogen II #status experimental <MAT2>  
F:19-379/DNA: HMW kininogen heavy chain #status experimental <HCH>  
F:19-131/DNA: HMW kininogen heavy chain #status experimental <CY1>  
F:142-253/DNA: cystatin homology <CY2>  
F:264-375/DNA: cystatin homology <CY3>  
F:380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>  
F:381-389/Product: bradykinin (kallidin I) #status experimental <BDY>  
F:390-644/DNA: HMW kininogen light chain #status experimental <LCH>  
F:421-510/Region: glycine/histidine/lysine-rich 30-residue repeats  
F:431-434/Product: low molecular weight growth factor #status experimental <GF>  
F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experim  
F:28-614,83-94,107-126,142-145,206-218,223-248,264-267,328-340,351-370/Disulfide bonds:  
F:48/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:142-253/Binding site: carboxylate (Asn) (covalent) #status experimental  
F:379-380/Cleavage site: Met-Lys (kallikrein) #status experimental  
F:383/Modified site: 4-hydroxyproline (Pro) (partial) #status experimental  
F:389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental  
F:401,533,542,546,557,571,593,628/Binding site: carboxylate (Thr) (covalent) #status ex  
F:577/Binding site: carboxylate (Ser) (covalent) #status experimental  
Query Match 90.0%; Score 618; DB 1; Length 644;  
Best Local Similarity 100.0%; Pred. No. 5.7e-50;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVGCPRDIPNTSPLESTLTHTITKLAENNAFFYFKIDNVKARQVY 62  
DB 253 GKDFVQPTKICVGCPRDIPNTSPLESTLTHTITKLAENNAFFYFKIDNVKARQVY 312  
QY 63 GKGYFDFVARETTCKSNELTESCTKLGQSLDCNAEVVVPWEKKIYPTV 118  
DB 313 GKGYFDFVARETTCKSNELTESCTKLGQSLDCNAEVVVPWEKKIYPTV 368  
RESULT 3  
KGBOL1  
N/A:kininogen, LMW I precursor - bovine  
N/Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen  
N/Contents: bradykinin (kallidin); kininogen I; kininogen II; prokininogen  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 22-Jun-1999  
C/Accession: A01283  
R:Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.  
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983  
A:Title: Primary structures of bovine liver low molecular weight kininogen precursors  
A:Reference number: A33984, MUID:83117859, PMID:6572010  
A:Accession: A01283  
A:Molecule type: mRNA  
A:Residues: 1-436 <NNA>  
A:Cross-references: GB:J00010; GR:V00426; NID:G163256; PID:AAA30604.1; PID:G163257  
C:Comment: The LMW kininogen precursor is produced from the same gene as the HMW form  
C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of  
C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator  
xyproline residue is present in the kininogen prior to the release of bradykinin.  
C:Superfamily: kininogen; cystatin homology  
C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; g  
F:1-18/DNA: signal sequence #status predicted <SIG>  
F:19-436/Product: LMW kininogen I #status predicted <MAT>  
F:19-378/Product: LMW kininogen I heavy chain #status predicted <HCH>  
F:19-130/DNA: cystatin homology <CY1>  
F:141-252/DNA: cystatin homology <CY2>  
F:263-374/DNA: cystatin homology <CY3>  
F:379-388/Product: lysyl-bradykinin (kallidin II) #status predicted <KBDY>  
F:380-388/Product: bradykinin (kallidin I) #status predicted <BDY>  
F:389-436/Product: LMW kininogen I light chain #status experimental <LCH>  
F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predic  
F:27-406,82-93,106-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bond  
F:47,87,168,169,197,204/Binding site: carboxylate (Asn) (covalent) #status predicted  
F:378-379/Cleavage site: Met-Lys (kallikrein) #status predicted  
F:382/Modified site: 4-hydroxyproline (Pro) #status predicted  
F:388-389/Cleavage site: Arg-Ser (kallikrein) #status predicted  
Query Match 64.0%; Score 440; DB 1; Length 436;  
Best Local Similarity 70.4%; Pred. No. 1.7e-33;  
Matches 81; Conservative 14; Mismatches 20; Indels 0; Gaps 0;  
QY 4 KDFVQPTKICVGCPRDIPNTSPLESTLTHTITKLAENNAFFYFKIDNVKARQVY 63  
DB 253 KDFVQPTKICVGCPRDIPNTSPLESTLTHTITKLAENNAFFYFKIDNVKARQVY 312  
QY 64 GKGYFDFVARETTCKSNELTESCTKLGQSLDCNAEVVVPWEKKIYPTV 118  
DB 313 GKGYFDFVARETTCKSNELTESCTKLGQSLDCNAEVVVPWEKKIYPTV 367  
RESULT 4  
KGBOL1  
N/A:kininogen, HMW I precursor - bovine  
N/Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen  
N/Contents: bradykinin (kallidin); kininogen I; kininogen II; prokininogen  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 22-Jun-1999  
C/Accession: A01281; A91923; A91938; A29559  
R:Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S.  
Nature 305, 545-549, 1983  
A:Title: A single gene for bovine high molecular weight and low molecular weight kin  
A:Reference number: A93317, MUID:84014106, PMID:6571899

A/Accession: A01281  
A/Molecule type: mRNA  
A/Residues: 1-621 <KIT>  
A/Cross-references: GB:V01491; GB:K01757; MID:9491; PIDN:CAA24735.1; PID:9492  
R/Kato, H.; Nagasawa, S.; Suzuki, T.  
J. Biochem. 67, 313-323, 1970  
A/Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and  
A/Reference number: A91923; MUID:70180420; PMID:4986212  
A/Accession: A91923  
A/Molecule type: protein  
A/Residues: 378-393 <KAT>  
R/Han, Y.N.; Komiya, M.; Iwanaga, S.; Suzuki, T.  
J. Biochem. 77, 55-68, 1975  
A/Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Am  
A/Reference number: A91938; MUID:75170265; PMID:1169237  
A/Accession: A91938  
A/Molecule type: protein  
A/Residues: 458-498 <KAN>  
R/Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Hayaehida, H.; Miyata, T.; Iwanaga,  
J. Biol. Chem. 262, 2768-2775, 1987  
A/Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of c  
A/Reference number: A92627; MUID:87137530; PMID:3546295  
A/Accession: A92627  
A/Molecule type: protein  
A/Residues: 120-123, 125-127, 129-378 <SUE>  
R/Lotsepich, F.; Kellermann, J.; Henschen, A.; Poertsch, B.; Muller-Esterl, W.  
Eur. J. Biochem. 152, 307-314, 1985  
A/Title: The amino acid sequence of the light chain of human high-molecular-mass kininog  
A/Reference number: A91533; MUID:86030270; PMID:4054110  
A/Contents: annotation: bovine cleavage sites; bovine carbohydrate binding sites  
R/Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.  
Seikagaku 56, 808, 1984  
A/Title: Disulfide bonds in bovine HMW kininogens.  
A/Reference number: A94300  
A/Contents: annotation; disulfide bonds  
A/Note: article in Japanese  
C/Comment: The HMW kininogen precursor is produced from the same gene as the LMW form as  
C/Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the  
C/Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is imp  
C/Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i  
C/Comment: Bradykinin residue is present in the kininogen prior to the release of bradykinin.  
C/Superfamily: kininogen; cystatin homology  
C/Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl  
P19-621/Domain: signal sequence #status predicted <SIG>  
P19-621/Product: HMW kininogen I #status predicted <MAT>  
P19-379/Product: HMW kininogen I heavy chain #status experimental <HCH>  
P19-130/Domain: cystatin homology <CY1>  
P141-252/Domain: cystatin homology <CY2>  
P141-252/Product: cystatin homology <CY2>  
P141-252/Domain: cystatin homology <CY3>  
P141-252/Product: cystatin homology <CY3>  
P137-386/Product: bradykinin (kallidin I) #status predicted <BDY>  
P137-386/Product: bradykinin (kallidin II) #status predicted <BDY>  
P137-386/Product: bradykinin (kallidin I) #status experimental <LCH>  
P137-386/Product: bradykinin (kallidin II) #status experimental <LCH>  
P127-404, 82-93, 106-125, 141-144, 205-217, 228-247, 261-264, 325-337, 348-367/Disulfide bonds:  
P127-404, 82-93, 106-125, 141-144, 205-217, 228-247, 261-264, 325-337, 348-367/Disulfide bonds:  
P137-377/Cleavage site: Met-Lys (kallikrein) #status predicted  
P137-377/Cleavage site: Met-Lys (kallikrein) #status predicted  
P138/Modified site: 4-hydroxyproline (Pro) #status predicted  
P138/Modified site: Arg-Ser (kallikrein) #status predicted  
P138-387/Cleavage site: Arg-Ser (kallikrein) #status predicted  
Query Match 64.0%; Score 440; DB 1; Length 621;  
Best Local Similarity 70.4%; Pred. No. 24e-33;  
Matches 81; Conservative 14; Mismatches 20; Indels 0; Gaps 0;  
OY 4 KDFVQPTKICVGPDPPTSPSELTITITKLAENNAATFPKIDNVKARVQV 63  
DB 253 KDFVQPTKICVGPDPPTSPSELTITITKLAENNAATFPKIDNVKARVQV 63

OY 64 GKQYFIDPVARETTCKSGNSBELTSCETKLGQSLDCNABVYVVPWEKKIYPTV 118  
DB 313 GLKYSIVFIARETTCKSGNSBELTSCETKLGQSLDCNABVYVVPWEKKIYPTV 367  
RESULT 5  
KGBOL2  
kininogen, LMW II precursor - bovine  
N/Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen  
N/Contents: bradykinin (kallidin); kininogen I; kininogen II; prokininogen  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 28-May-1999  
C/Accession: A01284  
R/Nawa, H.; Kitamura, N.; Hirose, T.; Asai, M.; Inayama, S.; Nakanishi, S.  
Proc. Natl. Acad. Sci. U.S.A. 80, 90-94, 1983  
A/Title: Primary structures of bovine liver low molecular weight kininogen precursor a  
A/Reference number: A91984; MUID:83117859; PMID:6572010  
A/Accession: A01284  
A/Molecule type: mRNA  
A/Residues: 1-434 <NAW>  
A/Cross-references: GB:V00427; GB:J00011; MID:9489; PIDN:CAA23710.1; PID:9490  
C/Comment: The LMW kininogen precursor is produced from the same gene as the HMW form a  
C/Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of th  
C/Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator,  
C/Comment: Bradykinin residue is present in the kininogen prior to the release of bradykinin.  
C/Superfamily: kininogen; cystatin homology  
C/Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; gly  
P19-434/Domain: signal sequence #status predicted <SIG>  
P19-434/Product: LMW kininogen II #status predicted <MAT>  
P19-130/Domain: cystatin homology <CY1>  
P141-252/Domain: cystatin homology <CY2>  
P141-252/Product: cystatin homology <CY2>  
P141-252/Domain: cystatin homology <CY3>  
P141-252/Product: cystatin homology <CY3>  
P137-386/Product: bradykinin (kallidin I) #status predicted <BDY>  
P137-386/Product: bradykinin (kallidin II) #status predicted <BDY>  
P137-386/Product: bradykinin (kallidin I) #status experimental <LCH>  
P137-386/Product: bradykinin (kallidin II) #status experimental <LCH>  
P127-404, 82-93, 106-125, 141-144, 205-217, 228-247, 261-264, 325-337, 348-367/Disulfide bonds:  
P127-404, 82-93, 106-125, 141-144, 205-217, 228-247, 261-264, 325-337, 348-367/Disulfide bonds:  
P137-377/Cleavage site: Met-Lys (kallikrein) #status predicted  
P137-377/Cleavage site: Met-Lys (kallikrein) #status predicted  
P138/Modified site: 4-hydroxyproline (Pro) #status predicted  
P138/Modified site: Arg-Ser (kallikrein) #status predicted  
P138-387/Cleavage site: Arg-Ser (kallikrein) #status predicted  
Query Match 60.1%; Score 413; DB 1; Length 434;  
Best Local Similarity 67.2%; Pred. No. 5.5e-31;  
Matches 78; Conservative 14; Mismatches 22; Indels 1; Gaps 1;  
OY 3 GKDFVQPTKICVGPDPPTSPSELTITITKLAENNAATFPKIDNVKARVQV 62  
DB 252 GKDFVQPTKICVGPDPPTSPSELTITITKLAENNAATFPKIDNVKARVQV 309  
OY 63 ACKYFIDPVARETTCKSGNSBELTSCETKLGQSLDCNABVYVVPWEKKIYPTV 118  
DB 310 GLKYSIVFIARETTCKSGNSBELTSCETKLGQSLDCNABVYVVPWEKKIYPTV 365  
RESULT 6  
KGBOL2  
kininogen, HMW II precursor - bovine  
N/Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen  
N/Contents: bradykinin (kallidin); kininogen I; kininogen II; prokininogen  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 14-Nov-1983 #sequence\_revision 14-Nov-1983 #text\_change 22-Jun-1999  
C/Accession: A01282; A91923; A91941; A91938; B29559  
R/Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, S.  
Nature 305, 545-549, 1983  
A/Title: A single gene for bovine high molecular weight and low molecular weight kininog  
A/Reference number: A93317; MUID:84014106; PMID:6571699  
A/Accession: A01282  
A/Molecule type: mRNA  
A/Residues: 1-619 <KIT>  
A/Cross-references: GB:V01492; GB:K01758; MID:9493; PIDN:CAA24736.1; PID:9494  
R/Kato, H.; Nagasawa, S.; Suzuki, T.

J. Biochem. 67, 313-323, 1970  
 A>Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds and  
 A/Reference number: A91923; MUID:70180420; PMID:4986212  
 A/Accession: A91923  
 A/Molecule type: Protein  
 A/Residues: 376-391 <Mat>  
 R/Han, Y.N.; Kato, H.; Iwanaga, S.; Suzuki, T.  
 J. Biochem. 79, 1201-1222, 1976  
 A>Title: Primary structure of bovine plasma high-molecular-weight kininogen. The amino  
 A/Reference number: A91941; MUID:76260155; PMID:956151  
 A/Accession: A91941  
 A/Molecule type: Protein  
 A/Residues: 387-455 <HAN>  
 A/Note: 398-Pro, 401-Val, and 455-Lys were also found  
 R/Han, Y.N.; Komiya, M.; Iwanaga, S.; Suzuki, T.  
 J. Biochem. 77, 55-68, 1975  
 A>Title: Studies on the primary structure of bovine high-molecular-weight kininogen. Amino  
 A/Reference number: A91938; MUID:75170265; PMID:1169237  
 A/Accession: A91938  
 A/Molecule type: Protein  
 A/Residues: 456-496 <HA2>  
 R/Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwanaga, S.  
 J. Biol. Chem. 262, 2768-2779, 1987  
 A>Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of  
 A/Reference number: A92627; MUID:87137530; PMID:3546295  
 A/Accession: B29859  
 A/Molecule type: Protein  
 A/Residues: 12, 20-104, 106-256, 257-376 <SUS>  
 R/Lottspeich, F.; Kallermann, J.; Henschen, A.; Foerbach, B.; Muller-Esterl, W.  
 Eur. J. Biochem. 152, 307-314, 1985  
 A>Title: The amino acid sequence of the light chain of human high-molecular-mass kininogen  
 A/Reference number: A91153; MUID:86030270; PMID:4054110  
 A/Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites  
 R/Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.  
 Seikagaku 56, 808, 1984  
 A>Title: Disulfide bonds in bovine HMW kininogens.  
 A/Reference number: A94300  
 A/Contents: annotation; disulfide bonds  
 A/Note: article in Japanese  
 C/Comment: The HMW kininogen precursor is produced from the same gene as the LMW form as  
 C/Comment: kininogen is a cysteine proteinase inhibitor, takes part in initiation of the  
 C/Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is imprecisely  
 C/Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, and  
 C/Comment: The residue is present in the kininogen prior to the release of bradykinin.  
 C/Superfamily: kininogen; cystatin homology  
 C/Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; duplication  
 F19-619/Product: HMW kininogen II #status predicted <SIG>  
 F19-376/Product: HMW kininogen II #status predicted <MAT>  
 F19-130/Domain: cystatin homology <CY1>  
 F141-252/Domain: cystatin homology <CY2>  
 F1261-372/Domain: cystatin homology <CY3>  
 F1377-386/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>  
 F1378-386/Product: bradykinin (kallidin I) #status experimental <BDY>  
 F1387-619/Product: HMW kininogen II light chain #status experimental <LCH>  
 F1418-488/Region: glycine/histidine/lysine-rich  
 F19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental  
 F27-589, 82-93, 106-125, 141-144, 205-217, 228-247, 261-264, 325-337, 348-367/Disulfide bonds:  
 F147/Binding site: carbohydrate (Asn) (covalent) #status absent  
 F167, 168, 169, 204, 280/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F136/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental  
 F197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental  
 F1376-377/Cleavage site: Met-Lys (kallikrein) #status experimental  
 F1380/Modified site: 4-hydroxyproline (pro) #status predicted  
 F1386-387/Cleavage site: Arg-Ser (kallikrein) #status experimental  
 F1396, 400, 404, 510/Binding site: carbohydrate (Ser) (covalent) #status experimental  
 F1397, 398, 518, 522, 534, 546, 551, 568/Binding site: carbohydrate (Thr) (covalent) #status experimental  
 F1496-497/Cleavage site: Arg-Thr (kallikrein) #status experimental

Query Match 60.1%; Score 413; DB 1; Length 619;  
 Best Local Similarity 67.2%; Pred. No. 8, 2e-31;  
 Matches 78; Conservative 14; Mismatches 22; Indels 2; Gaps 1;

QY 3 GKDFVQPTKICVGCPRDIPNTPSPLEETLTHITIKLNAENNATYFKIDNVKARVQV 62  
 DB 252 GEDFL--PPMVCVCPKIPVDSPLDEALNHSIAKLNAEHDGTFYFKIDTVKCATVQV 309  
 QY 63 AGKKYFIDPVARETTCSENEBELTSSCTKKLGQSLDCAVAVVVPWEKKIYPTV 118  
 DB 310 GGLKYSIVPIARETTCSENEBELTSSCTKKLGQSLDCAVAVVVPWEKKIYPTV 365

## RESULT 7

A28055

K-kininogen, LMW I precursor - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 20-Jun-1989 #sequence\_revision 20-Jun-1989 #text\_change 15-Nov-1996  
 C/Accession: A28055  
 R:Purico-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.  
 J. Biol. Chem. 260, 12054-12059, 1985  
 A>Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and  
 inhibitor.

A/Reference number: A92496; MUID:86008264; PMID:2413018

A/Accession: A28055

A/Molecule type: mRNA

A/Residues: 1-433 <PUR>

C/Superfamily: kininogen; cystatin homology

C/Keywords: alternative splicing

F19-433/Product: signal sequence #status predicted <SIG>

F19-131/Domain: K-kininogen, LMW I #status predicted <MAT>

F142-253/Domain: cystatin homology <CY2>

F1264-375/Domain: cystatin homology <CY3>

Query Match 59.7%; Score 410; DB 2; Length 433;  
 Best Local Similarity 66.4%; Pred. No. 1, 1e-30;  
 Matches 77; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVGCPRDIPNTPSPLEETLTHITIKLNAENNATYFKIDNVKARVQV 62  
 DB 253 GDDLPELLSPDCPCPNIPVDSPELKEALGHSIAQLNAENNATYFKIDTVKATSOV 312

QY 63 AGKKYFIDPVARETTCSENEBELTSSCTKKLGQSLDCAVAVVVPWEKKIYPTV 118  
 DB 313 AGTKYVIEPIARETTCSENEBELTSSCTKKLGQSLDCAVAVVVPWEKKIYPTV 368

## RESULT 8

A25486

kininogen, HMW I precursor - rat

N/Contents: bradykinin

C/Species: Rattus norvegicus (Norway rat)

C/Date: 08-Mar-1989 #sequence\_revision 08-Mar-1989 #text\_change 15-Nov-1996

R/Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.

J. Biol. Chem. 262, 2190-2198, 1987

A>Title: Differing expression patterns and evolution of the rat kininogen gene family.

A/Reference number: A92625; MUID:87137443; PMID:3029068

A/Accession: A25486

A/Molecule type: mRNA

A/Residues: 1-639 <KIT>

A/Note: the authors translated the codon CAA for residue 347 as Aen

C/Superfamily: kininogen; cystatin homology

C/Keywords: alternative splicing

F19-639/Product: signal sequence #status predicted <SIG>

F19-131/Domain: kininogen, HMW I #status predicted <MAT>

F142-253/Domain: cystatin homology <CY2>

F1264-375/Domain: cystatin homology <CY3>

Query Match 59.7%; Score 410; DB 2; Length 639;  
 Best Local Similarity 66.4%; Pred. No. 1, 1e-30;  
 Matches 77; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVGCPRDIPNTPSPLEETLTHITIKLNAENNATYFKIDNVKARVQV 62  
 DB 253 GDDLPELLSPDCPCPNIPVDSPELKEALGHSIAQLNAENNATYFKIDTVKATSOV 312





Furuto-Kato, S.; Matsumoto, A.; Kitamura, N.; Nakanishi, S.  
 J. Biol. Chem. 260, 12054-12059, 1985  
 A>Title: Primary structures of the mRNAs encoding the rat precursors for bradykinin and inhibitor.  
 A/Reference number: A92496; MUID:86008264; PMID:2413018  
 A/Accession: A01286  
 A/Molecule type: mRNA  
 A/Residues: 1-430 <PUB>  
 A/Cross-references: GB:M11883, NID:G205084; PID:G205085  
 R:Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.  
 J. Biol. Chem. 262, 2190-2198, 1987  
 A>Title: Differing expression patterns and evolution of the rat kininogen gene family.  
 A/Reference number: A92625; MUID:87137443; PMID:3029068  
 A/Accession: D25486  
 A/Molecule type: DNA  
 A/Residues: 375-430 <KIT>  
 R:Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.  
 J. Biol. Chem. 263, 973-979, 1988  
 A>Title: Purification and characterization of rat T-kininogens isolated from plasma of a rabbit.  
 A/Reference number: A92729; MUID:88087226; PMID:3121623  
 A/Accession: A28526  
 A/Molecule type: protein  
 A/Residues: E<sup>20-48</sup>; 376-430 <ENJ>  
 R:Xanda, S.; Sugiyama, K.; Takahashi, M.; Shumiyu, S.; Tomino, S.; Nagase, S.  
 Jpn. J. Cancer Res. 81, 63-68, 1990  
 A>Title: Identification of a protein increasing in serum of Nagase analbuminemic rats by immunoblotting.  
 A/Reference number: PLO193; MUID:90216390; PMID:2108948  
 A/Accession: PLO193  
 A/Molecule type: mRNA  
 A/Residues: 330-420, 'P' <KAN>  
 R:Anderson, K.P.; Croyle, M.L.; Lingrel, J.B.  
 Gene 81, 119-128, 1989  
 A>Title: Primary structure of a gene encoding rat T-kininogen.  
 A/Reference number: JQ0027; MUID:90034172; PMID:2806908  
 A/Accession: JQ0027  
 A/Molecule type: DNA  
 A/Residues: 1-60, E<sup>62-113</sup>, R<sup>115-165</sup>, P<sup>167-178</sup>, TKI<sup>182-211</sup>, P<sup>213-256</sup>, S<sup>258-388</sup>  
 R:Experimental source: strain Sprague-Dawley  
 R:Kagayama, R.; Kitamura, N.; Okubo, H.; Nakanishi, S.  
 J. Biol. Chem. 262, 2345-2351, 1987  
 A>Title: Differing utilization of homologous transcription initiation sites of rat K and X kininogen.  
 A/Reference number: A25488; MUID:87137465; PMID:3818598  
 A/Accession: B25488  
 A/Molecule type: preliminary  
 A/Status: preliminary  
 A/Residues: 1-48 <KAG>  
 A/Cross-references: GB:M14356, NID:G205090; PID:RAA41492.1; PID:G205091  
 R:Enjyoji, K.; Kato, H.; Hayashi, I.; Oh-ishi, S.; Iwanaga, S.  
 J. Biol. Chem. 263, 965-972, 1988  
 A>Title: Purification and characterization of two kinds of low molecular weight kininogen.  
 A/Reference number: A28525; MUID:88087225; PMID:3335530  
 A/Accession: A28525  
 A/Molecule type: protein  
 A/Residues: 376-430 <EN2>  
 R:Giorra, F.; Walter, R.; Vautravers, P.; Guilgoz, Y.  
 Arch. Biochem. Biophys. 322, 333-338, 1995  
 A>Title: Identification of several isoforms of T-kininogen expressed in the liver of aged rats.  
 A/Reference number: S68034; MUID:96032652; PMID:7574705  
 A/Accession: S68036  
 A/Molecule type: mRNA  
 A/Residues: 340-430 <SIS>  
 A/Experimental source: clone PSG17  
 A/Comment: At least three types of LMW kininogen precursors are present in rat plasma, coding bradykinin.  
 C/Comment: T-kininogens contain T-kinin (I-S-bradykinin), a novel kinin isolated after digestion of an Arg or Lys, it is probably not released from its precursor by either tissue or R.  
 C/Comment: The T-kininogens are produced in response to an inflammatory stimulant.  
 C/Genetics: 65/3, 102/3, 130/1, 187/3, 223/2, 252/1, 309/3, 345/3, 374/3, 398/3  
 A/Introns: 65/3, 102/3, 130/1, 187/3, 223/2, 252/1, 309/3, 345/3, 374/3, 398/3  
 C/Superfamily: kininogen; cystatin homology  
 C/Keywords: acute phase; bradykinin; cysteine proteinase inhibitor; duplication; glycoprotein  
 F:11-18/Domain: signal sequence #status predicted <SIG>  
 F:19-430/Product: T-kininogen I #status experimental <MAT>

F:19-130/Domain: cystatin homology <CY1>  
 F:141-252/Domain: cystatin homology <CY2>  
 F:263-374/Domain: cystatin homology <CY3>  
 F:378-386/Product: bradykinin #status predicted <BDY>  
 F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status expirime  
 F:82,126,168,204,326/Binding site: carboxylate (Asn) (covalent) #status predicted  
 F:83-94,107-125,141-144,205-217,228-247,263-266,327-339,350-369/Diulfide bonds: #statu  
 Query Match 55.3%, Score 380, DB 1, Length 430;  
 Best Local Similarity 62.1%, Pred. No. 6.7e-28;  
 Matches 72, Conservative 14, Mismatches 30, Indels 0, Gaps 0;  
 QY 3 GDFVQPTKLCVQCDPDTPTSPLEETLTITKLNANNATFYFKIDNVKARVQV 62  
 DB 252 GDLFLPLNRCGCPREIPVDSPELKALGHSIAQLAQNHNHIFYFKITVAKASQV 311  
 QY 63 AKKYPIDFVARETTCKSNBELTESCTKKLGSLDCNAEVTVVPEKKIYPTV 118  
 DB 312 AGVIIVIEFTARETNCOSKSTELTADCTHGLQSLNCNANVYMRPWKNVPTV 367  
 RESULT 13  
 UDBO  
 Cystatin - bovine  
 N/Alternate names: thiol proteinase inhibitor  
 C/Species: Bos primigenius taurus (cattle)  
 C/Date: 28-Feb-1986 #sequence\_revision 28-Feb-1986 #text\_change 06-Dec-1996  
 C/Accession: A01271  
 R:Hirado, M.; Teunassa, S.; Sakiyama, P.; Minobe, M.; Fujii, S.  
 FEBS Lett. 186, 41-45, 1985  
 A>Title: Complete amino acid sequence of bovine colostrum low-M-r cysteine proteinase I  
 A/Reference number: A01271; MUID:85231205; PMID:3891407  
 A/Accession: A01271  
 A/Molecule type: protein  
 A/Residues: 1-112 <HIR>  
 C/Superfamily: cystatin; cystatin homology  
 C/Keywords: colostrum; cysteine proteinase inhibitor  
 F:2-112/Domain: cystatin homology <CY>  
 F:48-52/Region: inhibitory #status predicted  
 F:66-76,90-110/Diulfide bonds: #status predicted  
 Query Match 20.0%, Score 137.5, DB 1, Length 112;  
 Best Local Similarity 28.8%, Pred. NO. 7.5e-06;  
 Matches 32, Conservative 25, Mismatches 35, Indels 19, Gaps 4;  
 QY 24 NSPELEETLTITKLNANNATFYFKIDNVKARVQVQVAGKYPIDFVARETTCKSN 83  
 DB 12 NEEGVQALSPAVSEFNKRNDAVQGRVVRVVRARQVQVSGMYPDLDELGRITCTK--S 69  
 QY 84 ESLTESC-----ETKLGSLDCNAEVTVVPEKKIYPTVTVNHWCE 126  
 DB 70 QANLSCFPNQLKREKL-----CSFQVYVVPWVN---TINLVKFSQ 111  
 RESULT 14  
 UDBO  
 Cystatin C precursor [validated] - human  
 N/Alternate names: gamma-CSP; gamma-trace; neuroendocrine basic polypeptide; post-gamm  
 C/Species: Homo sapiens (man)  
 C/Date: 06-Jul-1982 #sequence\_revision 31-Mar-1991 #text\_change 08-Dec-2000  
 C/Accession: S10216; S00004; J10095; A33400; S02751; A01270; A25434; S12288; A32732; A  
 R:Abrahamson, M.; Olafsson, I.; Paledottir, A.; Ulvabaeck, M.; Lundwall, A.; Jensen, (c  
 Biochem. J. 368, 287-294, 1990  
 A>Title: Structure and expression of the human cystatin C gene.  
 A/Reference number: S10216; MUID:90303202; PMID:2363674  
 A/Accession: S10216  
 A/Molecule type: DNA  
 A/Residues: 1-146 <ABL>  
 A/Cross-references: EMBL:X5255; NID:G30257; PID:CAA36497.1; PID:G296643  
 R:Abrahamson, M.; Grubb, A.; Olafsson, I.; Lundwall, A.  
 FEBS Lett. 216, 229-233, 1987  
 A>Title: Molecular cloning and sequence analysis of cDNA coding for the precursor of cl  
 A/Reference number: S00004; MUID:87219149; PMID:3495457

A/Accession: S00004  
A/Molecule type: mRNA  
A/Residues: 1-146 <AB>  
A/Cross-references: EMBL:X05607; NID:G30371; PIDN:CAA29096.1; PID:G755738  
R/Levy, E.; Lopez-Otin, C.; Ghiso, J.; Geltner, D.; Frangione, B.  
J. Exp. Med. 169, 1771-1778, 1989  
A/Title: Stroke in Icelandic patients with hereditary amyloid angiopathy is related to a  
A/Reference number: J00095; MUID:89235594; PMID:2541223  
A/Accession: J00095  
A/Molecule type: DNA  
A/Residues: 1-146 <LE>  
A/Cross-references: GB:X61691; NID:G30367; PIDN:CAA38956.2; PID:G4490944  
A/Note: The cystatin C gene isolated from the brain of an Icelandic patient with heredit  
e)  
R/Saitoh, E.; Sabatini, L.M.; Eddy, R.L.; Shows, T.B.; Azen, E.A.; Isemura, S.; Sanada,  
Biochem. Biophys. Res. Commun. 162, 1324-1331, 1989  
A/Title: The human cystatin C gene (CST3) is a member of the cystatin gene family which  
A/Reference number: A33400; MUID:89350949; PMID:2764935  
A/Accession: A33400  
A/Molecule type: DNA  
A/Residues: 1-24, T' 26-146 <BAI>  
A/Cross-references: GB:M27889; GB:M27890; GB:M27891; NID:G181385; PIDN:AA52164.1; PID:G  
R/Ghiso, J.; Cowan, N.; Frangione, B.  
Biol. Chem. Hoppe-Seyler 369, 205-208, 1988  
A/Title: Isolation of a sequence encoding human cystatin C. Conservation of exon-intron  
A/Reference number: 802751; MUID:89076507; PMID:3264504  
A/Accession: S02751  
A/Molecule type: DNA  
A/Residues: 82-119 <GH2>  
A/Cross-references: EMBL:M27769  
A/Note: The authors translated the codon ACC for residue 105 as Thr; the sequence shown  
R/Grubb, A.; Lofberg, H.  
Proc. Natl. Acad. Sci. U.S.A. 79, 3024-3027, 1982  
A/Title: Human gamma-trace, a basic microprotein: amino acid sequence and presence in th  
A/Reference number: A01270; MUID:82222268; PMID:6283552  
A/Accession: A01270  
A/Molecule type: protein  
A/Residues: 27-131, S' 133-146 <GRU>  
R/Ghiso, J.; Jensen, O.; Frangione, B.  
Proc. Natl. Acad. Sci. U.S.A. 83, 2974-2978, 1986  
A/Title: Amyloid fibrils in hereditary cerebral hemorrhage with amyloidosis of Iceland  
A/Reference number: A25434; MUID:86206076; PMID:3517880  
A/Accession: A25434  
A/Molecule type: protein  
A/Residues: 37-93, Q' 95-146 <GHI>  
R/Turk, V.; Brzin, J.; Longer, M.; Ritonja, A.; Eropkin, M.; Borchart, U.; Machleidt, W.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 1487-1496, 1983  
A/Title: Protein inhibitors of cysteine proteinases. III. Amino-acid sequence of cystati  
A/Reference number: 801461; MUID:84110059; PMID:6662498  
A/Accession: S12288  
A/Molecule type: protein  
A/Residues: 27-73 <TUR>  
R/Brzin, J.; Popovic, T.; Turk, V.  
Biochem. Biophys. Res. Commun. 118, 103-109, 1984  
A/Title: Human cystatin, a new protein inhibitor of cysteine proteinases.  
A/Reference number: A32732; MUID:84128015; PMID:6365094  
A/Accession: A32732  
A/Molecule type: protein  
A/Residues: 27-76 <BRZ>  
R/Olafsson, I.; Gudmundsson, G.; Abrahamson, M.; Jansson, O.; Grubb, A.  
Scand. J. Clin. Lab. Invest. 50, 85-93, 1990  
A/Title: The amino terminal portion of cerebrospinal fluid cystatin C in hereditary cyst  
A/Reference number: A60552; MUID:90193615; PMID:2315647  
A/Accession: A60552  
A/Molecule type: protein  
A/Residues: 27-49, XX' 52-64 <OLA>  
A/Note: This protein, purified from cerebrospinal fluid of patients with the autosomal  
R/Popovic, T.; Brzin, J.; Ritonja, A.; Turk, V.  
Biol. Chem. Hoppe-Seyler 371, 575-580, 1990  
A/Title: Different forms of human cystatin C.  
A/Reference number: S10607; MUID:91025625; PMID:2222856  
A/Accession: S10607  
A/Molecule type: protein

A/Molecule type: protein  
A/Residues: 27-53 <POP>  
A/Experimental source: urine, kidney disease  
A/Note: Truncated forms with amino ends at positions 35 and 36 of the precursor were ale  
R/Grubb, A.; Lofberg, H.; Barrett, A.G.  
FEBS Lett. 170, 370-374, 1984  
A/Title: The disulphide bridges of human cystatin C (gamma-trace) and chicken cystatin.  
A/Reference number: S01462  
A/Contents: annotation; disulfide bonds  
R/Berti, P.J.; Storer, A.C.  
Biochem. J. 302, 411-416, 1994  
A/Title: Local pH-dependent conformational changes leading to proteolytic susceptibility  
A/Reference number: S55305; MUID:94379969; PMID:8092991  
A/Accession: S55305  
A/Status: preliminary  
A/Molecule type: protein  
A/Residues: 27-49/106-146 <BR>  
C/Comment: This protein is found in the post-gamma-globulin fraction of cerebrospinal fl  
2 patients with certain autoimmune diseases.  
C/Comment: This protein is an inhibitor of cysteine proteinases and may serve an importa  
C/Comment: A mutant cystatin C, with 94-Gln, is deposited in hereditary cerebral hermoz  
C/Genetics:  
A/Gene: GDB:CST3  
A/Cross-references: GDB:119817; OMIM:105150  
A/Map position: 20p11.2-20p11.2  
A/Introns: 81/3; 119/3  
C/Superfamily: cystatin; cystatin homology  
C/Keywords: amyloid; cysteine proteinase inhibitor; extracellular protein; hydroxyprolin  
P1-26/Domain: signal; cysteine proteinase predicted <SIG>  
P27-146/Product: cystatin C #status experimental <MAT>  
P35-146/Domain: cystatin homology <CYS>  
P81-85/Region: inhibitory status predicted  
P79/Modified site: hydroxyproline (pro) (partial) #status experimental  
P109-109,123-143/Disulfide bonds: #status experimental  
Query Match 19.34; Score 132.5; DB 1; Length 146;  
Best Local Similarity 27.04; Pred. No. 2.9e-05;  
Matches 33; Conservative 25; Mismatches 53; Indels 11; Gaps 4;  
OY 8 QPTKICVGCPRDPTNSPLETLTHITKLNAENATFYFKIDNVKARVQVACKY 67  
DB 31 KPFR--LVGGPNDASVEEGVRAALDPANVEYNKASNDYHSRALQVRAKQIVAGVY 88  
OY 68 FIDFVARETTCKSKSNELTSC---ETKKLGSLDCNAEVTVVWPKKIYPTVTHWE 124  
DB 89 FIDVGLGRITCTT--TQFNLDNCFPHDQPHKRAKAPCSQIYAVPMQ----GTMILSKST 142  
OY 125 CE 126  
DB 143 CQ 144  
RESULT 15  
S07085  
cystatin C precursor - rat (fragment)  
C/Species: Rattus norvegicus (Norway rat)  
C/Data: 01-Dec-1993 #sequence revision 03-Aug-1995 #text\_change 16-Jul-1999  
A/Accession: S07085; MUID:9337; G3109  
R/Cole, T.; Dickson, F.W.; Enard, P.; Averill, S.; Riebringer, G.P.; Gauthier, F.; Schre  
Eur. J. Biochem. 186, 35-42, 1989  
A/Title: The cDNA structure and expression analysis of the genes for the cysteine protein  
A/Reference number: S07085; MUID:90092122; PMID:2689174  
A/Accession: S07085  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-127 <COI>  
A/Cross-references: EMBL:X16957; NID:G56043; PIDN:CAA34831.1; PID:G736290  
R/Enard, A.; Enard, P.; Paucher, D.; Gauthier, P.  
FEBS Lett. 236, 475-478, 1988  
A/Title: Two rat homologues of human cystatin C.  
A/Reference number: S01337; MUID:88313020; PMID:3044831  
A/Accession: S01337  
A/Molecule type: protein



A:Residues: 8-49 <ESN>  
 R:Enard, A.; Enard, F.; Guillou, F.; Gauthier, F.  
 PDBS Lett. 300, 131-135, 1992  
 A:Title: Production of the cysteine proteinase inhibitor cystatin C by rat Sertoli cells  
 A:Reference number: S21109, MUID:92225121, PMID:1563513  
 A:Accession: S21109

A:Molecule type: protein  
 A:Residues: 8, 'XX', 11-20 <ES2>  
 C:Superfamily: cystatin; cystatin homology  
 C:Keywords: cysteine proteinase inhibitor  
 F:15-127/Domain: cystatin homology <CYS>  
 F:80-90, 104-124/Disulfide bonds: #status predicted

Query Match 18.9%; Score 130; DB 2; Length 127;  
 Best Local Similarity 28.0%; Pred. No. 4.3e-05;  
 Matches 30; Conservative 28; Mismatches 43; Indels 6; Gaps 4;

|    |    |  |     |
|----|----|--|-----|
| Oy | 8  | QPTKICVGPDRDIPITNSPELEETLTHITKLNAENNAFFPKIDNVKARVQVYVAGKY  | 67  |
| Db | 11 | RPPRL-LGAPQADASEEGVQRALDFAVSEYNGKSGNDAYHGRATQWVRARQLVAGINY | 69  |
| Oy | 68 | FIDFVARETTCSKESNELTSC---ETKLGOSLDCNAEVVYVWPE               | 111 |
| Db | 70 | YLDVENGRTCTK-SQTNLT-NCPFDQPHLRKALCSFOISVPEWK               | 114 |

Search completed: September 24, 2004, 14:10:49  
 Job time : 14.716 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 24, 2004, 14:08:41, Search time 44.704 Seconds  
(without alignments)  
913.519 Million cell updates/sec

Title: US-10-661-784-3

Perfect score: 687

Sequence: 1 GSGKDFVQPTKICVGCPRD.....VPMKKIYPTVTVNHECEP 127

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1349238 seqs, 321558718 residues

Total number of hits satisfying chosen parameters: 1349238

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: Published Applications AA:

1: /cgn2\_6/ptodata/1/pubpaas/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaas/PCT\_NEW\_PUB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaas/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaas/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaas/US07\_NEW\_PUB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaas/PCTUS\_PUBCOMB.pep.\*  
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10: /cgn2\_6/ptodata/1/pubpaas/US09B\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/1/pubpaas/US09C\_PUBCOMB.pep.\*  
12: /cgn2\_6/ptodata/1/pubpaas/US09\_NEW\_PUB.pep.\*  
13: /cgn2\_6/ptodata/1/pubpaas/US10A\_PUBCOMB.pep.\*  
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16: /cgn2\_6/ptodata/1/pubpaas/US10\_NEW\_PUB.pep.\*  
17: /cgn2\_6/ptodata/1/pubpaas/US60\_NEW\_PUB.pep.\*  
18: /cgn2\_6/ptodata/1/pubpaas/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description       |
|------------|-------|-------------|--------|----|-------------------|
| 1          | 618   | 90.0        | 390    | 15 | US-10-162-335-82  |
| 2          | 618   | 90.0        | 398    | 15 | US-10-162-335-70  |
| 3          | 618   | 90.0        | 427    | 10 | US-09-919-039-29  |
| 4          | 618   | 90.0        | 615    | 15 | US-10-162-335-72  |
| 5          | 618   | 90.0        | 644    | 15 | US-10-162-335-74  |
| 6          | 618   | 90.0        | 644    | 15 | US-10-162-335-84  |
| 7          | 381   | 55.5        | 424    | 14 | US-10-316-253-217 |
| 8          | 380   | 55.3        | 430    | 14 | US-10-316-253-215 |
| 9          | 163.5 | 23.8        | 145    | 14 | US-10-329-428-2   |
| 10         | 163.5 | 23.8        | 197    | 10 | US-09-746-783-197 |
| 11         | 163   | 23.7        | 178    | 9  | US-09-969-834-1   |
| 12         | 138.5 | 20.2        | 121    | 9  | US-09-775-932-14  |
| 13         | 138.5 | 20.2        | 128    | 9  | US-09-775-932-12  |
| 14         | 138.5 | 20.2        | 149    | 9  | US-09-940-497-2   |
| 15         | 137.5 | 20.0        | 112    | 8  | US-08-849-303-16  |

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|----|-------|------|-----|----|--------------------|
| 16 | 137.5 | 20.0 | 112 | 16 | US-10-655-136-16   |
| 17 | 136.5 | 19.9 | 118 | 9  | US-09-775-932-24   |
| 18 | 132.5 | 19.3 | 120 | 9  | US-09-775-932-2    |
| 19 | 132.5 | 19.3 | 120 | 16 | US-10-695-194-2    |
| 20 | 132.5 | 19.3 | 146 | 8  | US-08-849-303-17   |
| 21 | 132.5 | 19.3 | 146 | 9  | US-09-940-497-3    |
| 22 | 132.5 | 19.3 | 146 | 9  | US-09-969-834-3    |
| 23 | 132.5 | 19.3 | 146 | 14 | US-10-329-428-3    |
| 24 | 132.5 | 19.3 | 146 | 14 | US-10-376-564-47   |
| 25 | 132.5 | 19.3 | 146 | 16 | US-10-655-136-17   |
| 26 | 132.5 | 19.3 | 146 | 16 | US-10-695-194-1    |
| 27 | 132.5 | 19.3 | 249 | 16 | US-10-257-384-4    |
| 28 | 132.5 | 19.3 | 641 | 16 | US-10-257-384-2    |
| 29 | 131.5 | 19.1 | 317 | 12 | US-10-210-172-86   |
| 30 | 131.5 | 19.1 | 345 | 12 | US-10-210-172-86   |
| 31 | 131.5 | 19.1 | 356 | 12 | US-10-210-172-84   |
| 32 | 131.5 | 19.1 | 369 | 12 | US-10-210-172-78   |
| 33 | 131.5 | 19.1 | 369 | 12 | US-10-210-172-80   |
| 34 | 131.5 | 19.1 | 382 | 12 | US-10-315-664-93   |
| 35 | 131.5 | 19.1 | 382 | 12 | US-09-978-360A-425 |
| 36 | 130   | 18.9 | 127 | 8  | US-08-849-303-19   |
| 37 | 130   | 18.9 | 127 | 16 | US-10-655-136-19   |
| 38 | 129.5 | 18.9 | 140 | 14 | US-10-376-564-46   |
| 39 | 129.5 | 18.9 | 140 | 14 | US-10-376-564-48   |
| 40 | 128   | 18.6 | 111 | 8  | US-08-849-303-25   |
| 41 | 128   | 18.6 | 111 | 16 | US-10-655-136-26   |
| 42 | 127.5 | 18.6 | 140 | 8  | US-08-849-303-18   |
| 43 | 127.5 | 18.6 | 140 | 16 | US-10-655-136-18   |
| 44 | 124.5 | 18.1 | 121 | 9  | US-09-775-932-8    |
| 45 | 124.5 | 18.1 | 141 | 8  | US-08-849-303-24   |

#### ALIGNMENTS

#### RESULT 1

US-10-162-335-82  
Sequence 82, Application US/10162335  
Publication No. US20040009480A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, David W.  
APPLICANT: Baumgartner, Jason C.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Gangolli, Esha A.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Gorman, Linda  
APPLICANT: Guo, Xiaojia (Sasha)  
APPLICANT: Hjal, Tord  
APPLICANT: Kakuda, Ramesh  
APPLICANT: Li, Li  
APPLICANT: MacDougall, John R.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Millet, Isabelle  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Patturajan, Meera  
APPLICANT: Pena, Carol E. A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Shimketa, Richard A.  
APPLICANT: Stone, David J.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Vose, Edward Z.  
APPLICANT: Zerkusen, Bryan D.  
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Met  
FILE REFERENCE: 21402-377 B  
CURRENT APPLICATION NUMBER: US/10162,335  
CURRENT FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: 60/295,607  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/295,651  
PRIOR FILING DATE: 2001-06-04

Sequence 16, Appl  
Sequence 24, Appl  
Sequence 2, Appl  
Sequence 17, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 3, Appl  
Sequence 47, Appl  
Sequence 17, Appl  
Sequence 1, Appl  
Sequence 4, Appl  
Sequence 2, Appl  
Sequence 82, Appl  
Sequence 86, Appl  
Sequence 84, Appl  
Sequence 80, Appl  
Sequence 93, Appl  
Sequence 425, Appl  
Sequence 19, Appl  
Sequence 19, Appl  
Sequence 46, Appl  
Sequence 48, Appl  
Sequence 26, Appl  
Sequence 26, Appl  
Sequence 18, Appl  
Sequence 8, Appl  
Sequence 24, Appl

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/ PRIOR APPLICATION NUMBER: 60/296,404
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 60/296,418
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 60/297,414
/ PRIOR FILING DATE: 2001-06-11
/ PRIOR APPLICATION NUMBER: 60/297,567
/ PRIOR FILING DATE: 2001-06-12
/ PRIOR APPLICATION NUMBER: 60/298,285
/ PRIOR FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 60/298,556
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/299,949
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: 60/300,883
/ PRIOR FILING DATE: 2001-06-26
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 201
/ SEQ ID NO 82
/ LENGTH: 390
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-162-335-82

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Best Local Similarity 100.0%; Pred. No. 5.7e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 216 GKDFVQPTKICVCGPRDIPITNSPELEETLTHITKLAENNAATFYFKIDNVKARVQV 275

QY 63 AGKKYFIDFVARETTCKESNEBELTSCETKLGOSLDCNAEVVVPWEKKIYPTV 118
DB 276 AGKKYFIDFVARETTCKESNEBELTSCETKLGOSLDCNAEVVVPWEKKIYPTV 331

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RESULT 2
US-10-162-335-70
/ Sequence 70, Application US/10162335
/ Publication No. US2004009480A1
/ GENERAL INFORMATION:
/ APPLICANT: Anderson, David W.
/ APPLICANT: Baumgartner, Jason C.
/ APPLICANT: Boldog, Ferenc L.
/ APPLICANT: Casman, Stacie J.
/ APPLICANT: Edinger, Shlomit R.
/ APPLICANT: Gangoli, Zasha A.
/ APPLICANT: Gerlach, Valerie
/ APPLICANT: Gorman, Linda
/ APPLICANT: Guo, Xieojia (Sasha)
/ APPLICANT: Hjal, Tord
/ APPLICANT: Kekuda, Rameesh
/ APPLICANT: Li, Li
/ APPLICANT: MacDougall, John R.
/ APPLICANT: Malyankar, Uriel M.
/ APPLICANT: Millet, Isabelle
/ APPLICANT: Padigaru, Muralidhara
/ APPLICANT: Parturajan, Meera
/ APPLICANT: Pena, Carol E. A.
/ APPLICANT: Restelli, Luca
/ APPLICANT: Shimkete, Richard A.
/ APPLICANT: Stone, David J.
/ APPLICANT: Sytek, Kimberly A.
/ APPLICANT: Vernet, Corine A. M.
/ APPLICANT: Voss, Edward Z.
/ APPLICANT: Zernhusen, Bryan D.
/ TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method
/ FILE REFERENCE: 21402-377 B
/ CURRENT APPLICATION NUMBER: US/10/162,335
/ PRIOR FILING DATE: 2002-10-01
/ PRIOR APPLICATION NUMBER: 60/295,607
/ PRIOR FILING DATE: 2001-06-04

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/ PRIOR APPLICATION NUMBER: 60/295,661
/ PRIOR FILING DATE: 2001-06-04
/ PRIOR APPLICATION NUMBER: 60/296,404
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 60/296,418
/ PRIOR FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 60/297,414
/ PRIOR FILING DATE: 2001-06-11
/ PRIOR APPLICATION NUMBER: 60/297,567
/ PRIOR FILING DATE: 2001-06-12
/ PRIOR APPLICATION NUMBER: 60/298,285
/ PRIOR FILING DATE: 2001-06-14
/ PRIOR APPLICATION NUMBER: 60/298,556
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/299,949
/ PRIOR FILING DATE: 2001-06-21
/ PRIOR APPLICATION NUMBER: 60/300,883
/ PRIOR FILING DATE: 2001-06-26
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 201
/ SEQ ID NO 70
/ LENGTH: 398
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-162-335-70

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Query Match          90.0%; Score 618; DB 15; Length 398;
Best Local Similarity 100.0%; Pred. No. 5.8e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVCGPRDIPITNSPELEETLTHITKLAENNAATFYFKIDNVKARVQV 62
DB 224 GKDFVQPTKICVCGPRDIPITNSPELEETLTHITKLAENNAATFYFKIDNVKARVQV 283

QY 63 AGKKYFIDFVARETTCKESNEBELTSCETKLGOSLDCNAEVVVPWEKKIYPTV 118
DB 284 AGKKYFIDFVARETTCKESNEBELTSCETKLGOSLDCNAEVVVPWEKKIYPTV 339

RESULT 3
US-09-919-039-29
/ Sequence 29, Application US/09919039
/ Publication No. US20030108871A1
/ GENERAL INFORMATION:
/ APPLICANT: Kasai, Matthew R.
/ TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
/ FILE REFERENCE: PA-0035 US
/ CURRENT APPLICATION NUMBER: US/09/919,039
/ PRIOR FILING DATE: 2002-09-09
/ PRIOR APPLICATION NUMBER: 60/222,113
/ PRIOR FILING DATE: 2000-07-28
/ NUMBER OF SEQ ID NOS: 401
/ SOFTWARE: PERL Program
/ SEQ ID NO 29
/ LENGTH: 427
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. US20030108871A1 167507CD1
US-09-919-039-29

```

```

Query Match          90.0%; Score 618; DB 10; Length 427;
Best Local Similarity 100.0%; Pred. No. 6.4e-59;
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GKDFVQPTKICVCGPRDIPITNSPELEETLTHITKLAENNAATFYFKIDNVKARVQV 62
DB 253 GKDFVQPTKICVCGPRDIPITNSPELEETLTHITKLAENNAATFYFKIDNVKARVQV 312

QY 63 AGKKYFIDFVARETTCKESNEBELTSCETKLGOSLDCNAEVVVPWEKKIYPTV 118
DB 313 AGKKYFIDFVARETTCKESNEBELTSCETKLGOSLDCNAEVVVPWEKKIYPTV 368

```

## RESULT 4

US-10-162-335-72  
Sequence 72, Application US/10162335  
Publication No. US20040009480A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, David W.  
APPLICANT: Baumgartner, Jason C.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Gangolli, Esha A.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Gorman, Linda  
APPLICANT: Guo, Xiaojia (Sasha)  
APPLICANT: Hjal, Tord  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Li, Li  
APPLICANT: MacDougall, John R.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Millet, Isabelle  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Patturajan, Meera  
APPLICANT: Pena, Carol E. A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Stone, David J.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Voss, Edward Z.  
APPLICANT: Zerhusen, Bryan D.  
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method  
FILE REFERENCE: 21402-377 B  
CURRENT APPLICATION NUMBER: US/10/162.335  
CURRENT FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: 60/295,607  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/295,661  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/296,404  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/296,418  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/297,414  
PRIOR FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 60/297,567  
PRIOR FILING DATE: 2001-06-12  
PRIOR APPLICATION NUMBER: 60/298,285  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: 60/298,556  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/299,949  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: 60/300,883  
PRIOR FILING DATE: 2001-06-26  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 201  
SEQ ID NO 72  
LENGTH: 615  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-162-335-72

Query Match 90.0%; Score 618; DB 15; Length 615;  
Best Local Similarity 100.0%; Pred. No. 1e-58;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GKDFVQPTKICVGCPRDPTNSPELETLTHITKLNANNATFYFKIDNVKARVQV 62  
DB 224 GKDFVQPTKICVGCPRDPTNSPELETLTHITKLNANNATFYFKIDNVKARVQV 283  
QY 63 AGKYPIDFVARETTCSEKESBELTESCTKKGQSLDCNAEVVYVWPKIYPTV 118

DB 284 AGKYPIDFVARETTCSEKESBELTESCTKKGQSLDCNAEVVYVWPKIYPTV 339

## RESULT 5

US-10-162-335-74  
Sequence 74, Application US/10162335  
Publication No. US20040009480A1  
GENERAL INFORMATION:  
APPLICANT: Anderson, David W.  
APPLICANT: Baumgartner, Jason C.  
APPLICANT: Boldog, Ferenc L.  
APPLICANT: Casman, Stacie J.  
APPLICANT: Edinger, Shlomit R.  
APPLICANT: Gangolli, Esha A.  
APPLICANT: Gerlach, Valerie  
APPLICANT: Gorman, Linda  
APPLICANT: Guo, Xiaojia (Sasha)  
APPLICANT: Hjal, Tord  
APPLICANT: Kekuda, Ramesh  
APPLICANT: Li, Li  
APPLICANT: MacDougall, John R.  
APPLICANT: Malyankar, Uriel M.  
APPLICANT: Millet, Isabelle  
APPLICANT: Padigaru, Muralidhara  
APPLICANT: Patturajan, Meera  
APPLICANT: Pena, Carol E. A.  
APPLICANT: Rastelli, Luca  
APPLICANT: Shimkets, Richard A.  
APPLICANT: Stone, David J.  
APPLICANT: Spytek, Kimberly A.  
APPLICANT: Vernet, Corine A. M.  
APPLICANT: Voss, Edward Z.  
APPLICANT: Zerhusen, Bryan D.  
TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method  
FILE REFERENCE: 21402-377 B  
CURRENT APPLICATION NUMBER: US/10/162.335  
CURRENT FILING DATE: 2002-10-01  
PRIOR APPLICATION NUMBER: 60/295,607  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/295,661  
PRIOR FILING DATE: 2001-06-04  
PRIOR APPLICATION NUMBER: 60/296,404  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/296,418  
PRIOR FILING DATE: 2001-06-06  
PRIOR APPLICATION NUMBER: 60/297,414  
PRIOR FILING DATE: 2001-06-11  
PRIOR APPLICATION NUMBER: 60/297,567  
PRIOR FILING DATE: 2001-06-12  
PRIOR APPLICATION NUMBER: 60/298,285  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: 60/298,556  
PRIOR FILING DATE: 2001-06-15  
PRIOR APPLICATION NUMBER: 60/299,949  
PRIOR FILING DATE: 2001-06-21  
PRIOR APPLICATION NUMBER: 60/300,883  
PRIOR FILING DATE: 2001-06-26  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 201  
SEQ ID NO 74  
LENGTH: 644  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-162-335-74

Query Match 90.0%; Score 618; DB 15; Length 644;  
Best Local Similarity 100.0%; Pred. No. 1.1e-58;  
Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 GKDFVQPTKICVGCPRDPTNSPELETLTHITKLNANNATFYFKIDNVKARVQV 62  
DB 253 GKDFVQPTKICVGCPRDPTNSPELETLTHITKLNANNATFYFKIDNVKARVQV 312

OY 63 AGKKYFIDFVARETTCSKESNEELTSCETKKGSLDCAAEVTVVWPKKIYPTV 118  
 DB 313 AGKKYFIDFVARETTCSKESNEELTSCETKKGSLDCAAEVTVVWPKKIYPTV 368

## RESULT 6

US-10-162-335-84  
 ; Sequence 84, Application US/10162335  
 ; Publication No. US2004000980A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, David W.  
 ; APPLICANT: Baumgartner, Jason C.  
 ; APPLICANT: Boldog, Ferenc L.  
 ; APPLICANT: Casman, Stacie J.  
 ; APPLICANT: Edinger, Shlomit R.  
 ; APPLICANT: Gangolli, Zeba A.  
 ; APPLICANT: Gerlach, Valerie  
 ; APPLICANT: Gorman, Linda  
 ; APPLICANT: Guo, Xiaojia (Sasha)  
 ; APPLICANT: Hjalte, Torle  
 ; APPLICANT: Kekuda, Rameesh  
 ; APPLICANT: Li, Li  
 ; APPLICANT: MacDougall, John R.  
 ; APPLICANT: Malyankar, Uriel M.  
 ; APPLICANT: Millet, Isabelle  
 ; APPLICANT: Padigaru, Muralidhara  
 ; APPLICANT: Patturajan, Meera  
 ; APPLICANT: Pena, Carol E. A.  
 ; APPLICANT: Rastelli, Luca  
 ; APPLICANT: Shimkets, Richard A.  
 ; APPLICANT: Stone, David J.  
 ; APPLICANT: Spytek, Kimberly A.  
 ; APPLICANT: Vernet, Corina A. M.  
 ; APPLICANT: Voss, Edward Z.  
 ; APPLICANT: Zetser, Bryan D.  
 ; TITLE OF INVENTION: Therapeutic Polypeptides, Nucleic Acids Encoding Same, and Method  
 ; FILE REFERENCE: 21402-377 B  
 ; CURRENT APPLICATION NUMBER: US/10/162,335  
 ; PRIOR FILING DATE: 2002-10-01  
 ; PRIOR APPLICATION NUMBER: 60/295,607  
 ; PRIOR FILING DATE: 2001-06-04  
 ; PRIOR APPLICATION NUMBER: 60/295,661  
 ; PRIOR FILING DATE: 2001-06-04  
 ; PRIOR APPLICATION NUMBER: 60/296,404  
 ; PRIOR FILING DATE: 2001-06-06  
 ; PRIOR APPLICATION NUMBER: 60/296,418  
 ; PRIOR FILING DATE: 2001-06-06  
 ; PRIOR APPLICATION NUMBER: 60/297,414  
 ; PRIOR FILING DATE: 2001-06-11  
 ; PRIOR APPLICATION NUMBER: 60/297,567  
 ; PRIOR FILING DATE: 2001-06-12  
 ; PRIOR APPLICATION NUMBER: 60/298,285  
 ; PRIOR FILING DATE: 2001-06-14  
 ; PRIOR APPLICATION NUMBER: 60/298,556  
 ; PRIOR FILING DATE: 2001-06-15  
 ; PRIOR APPLICATION NUMBER: 60/299,949  
 ; PRIOR FILING DATE: 2001-06-21  
 ; PRIOR APPLICATION NUMBER: 60/300,883  
 ; PRIOR FILING DATE: 2001-06-26  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 201  
 ; SEQ ID NO 84  
 ; LENGTH: 644  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-162-335-84

Query Match 90.0%; Score 618; DB 15; Length 644;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-58;  
 Matches 116; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 3 GKDFVPPPTKICVCGPRDPTNSPELEBTLTHITTKLAENNAFFYFKIDNVKARQV 62

DB 253 GKDFVPPPTKICVCGPRDPTNSPELEBTLTHITTKLAENNAFFYFKIDNVKARQV 312  
 OY 63 AGKKYFIDFVARETTCSKESNEELTSCETKKGSLDCAAEVTVVWPKKIYPTV 118  
 DB 313 AGKKYFIDFVARETTCSKESNEELTSCETKKGSLDCAAEVTVVWPKKIYPTV 368

## RESULT 7

US-10-316-253-217  
 ; Sequence 217, Application US/10316253  
 ; Publication No. US20030162706A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Procter & Gamble Company  
 ; APPLICANT: Peters, Kevin  
 ; APPLICANT: Thompson, Larry  
 ; APPLICANT: Wang, Peng  
 ; APPLICANT: Greis, Kenneth  
 ; TITLE OF INVENTION: Angiogenesis Modulating Proteins  
 ; FILE REFERENCE: 8865M  
 ; CURRENT APPLICATION NUMBER: US/10/316,253  
 ; PRIOR FILING DATE: 2002-12-10  
 ; PRIOR APPLICATION NUMBER: US 60/355,295  
 ; PRIOR FILING DATE: 2002-02-08  
 ; NUMBER OF SEQ ID NOS: 308  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 217  
 ; LENGTH: 424  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-10-316-253-217

Query Match 55.5%; Score 381; DB 14; Length 424;  
 Best Local Similarity 62.1%; Pred. No. 5.8e-33;  
 Matches 72; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

OY 3 GKDFVPPPTKICVCGPRDPTNSPELEBTLTHITTKLAENNAFFYFKIDNVKARQV 62  
 DB 246 GDDLPELLPNCRCGCPREIPVDSPELKEALGHSLAQLNAQHNHIFYFKIDTVKATQV 305

OY 63 AGKKYFIDFVARETTCSKESNEELTSCETKKGSLDCAAEVTVVWPKKIYPTV 118  
 DB 306 AGVIVVIEFIARETNCQSKQSKTDLTADCTEKLHGLSLDCAAEVTVVWPKKIYPTV 361

## RESULT 8

US-10-316-253-215  
 ; Sequence 215, Application US/10316253  
 ; Publication No. US20030162706A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Procter & Gamble Company  
 ; APPLICANT: Peters, Kevin  
 ; APPLICANT: Thompson, Larry  
 ; APPLICANT: Wang, Peng  
 ; APPLICANT: Greis, Kenneth  
 ; TITLE OF INVENTION: Angiogenesis Modulating Proteins  
 ; FILE REFERENCE: 8865M  
 ; CURRENT APPLICATION NUMBER: US/10/316,253  
 ; PRIOR FILING DATE: 2002-12-10  
 ; PRIOR APPLICATION NUMBER: US 60/355,295  
 ; PRIOR FILING DATE: 2002-02-08  
 ; NUMBER OF SEQ ID NOS: 308  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 215  
 ; LENGTH: 430  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-10-316-253-215

Query Match 55.3%; Score 380; DB 14; Length 430;  
 Best Local Similarity 62.1%; Pred. No. 7.7e-33;  
 Matches 72; Conservative 14; Mismatches 30; Indels 0; Gaps 0;

|     |    |   |     |
|-----|----|---|-----|
| 3   | QY | QKQVQPPQTKICVCGPRDIPNTPNSPELBETLTHITKNAENNATPYFKLNNVKQARVOVV  | 62  |
| 252 | DB | GODFELLPPKNCRCGCPREIPVDSPELKEALGHSIAQLNACHNHRIPYFKIDTVKCAEQVV | 311 |
| 63  | QY | AGKKYPFDVARETTCKGSESNBEETSCETCKLQGLQSLCNAEYVVVVPWEKKIYPTV     | 118 |
| 312 | DB | AGVTVYIEPTARNGSKOSKTELTADCETKHGLGSLCNAVYVVRPWENKVVPTV         | 367 |

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RESULT 9
US-10-329-428-2
Sequence 2, Application US/10329428
Publication No. US20030114646A1
GENERAL INFORMATION:
APPLICANT: LI, et al.
TITLE OF INVENTION: Human Cystatin P
FILE REFERENCE: P7269102
CURRENT APPLICATION NUMBER: US/10/329,428
CURRENT FILING DATE: 2002-12-27
PRIOR APPLICATION NUMBER: 60/014,795
PRIOR FILING DATE: 1996-04-03
PRIOR APPLICATION NUMBER: 08/832,535
PRIOR FILING DATE: 1997-04-03
PRIOR APPLICATION NUMBER: 09/019,485
PRIOR FILING DATE: 1998-01-29
PRIOR APPLICATION NUMBER: 09/528,436
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent in version 3.2
SEQ ID NO 2
LENGTH: 145
TYPE: PRT
ORGANISM: Homo sapiens
US-10-329-428-2

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Query Match      23.8%; Score 163.5; DB 14; Length 145;
Best Local Similarity 31.6%; Pred. No. 5.7e-10;
Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;

Qy      11 TKICVCGPRDIPTPNGPELEETLTTHTTKLNAENATTFPKIDNKKARVQVWAGKKYIFD 70
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      32 SRVFGPGPKTKINDPGVLOAARSVEKFPKNCNDNMLTFKESRITRALVQIVKGLKLYLE 91

Qy      71 FVARETTTCSKESNEELTESCS----TKKLGSLDCAAEVYVFWPEKKIYPTVTVHWHS 124
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      92 VEIGRTTCKNQHRLR--DDCFQFNTHLTKTSSCYSEVWVFW-----LQSPFE 138

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RESULT 10  
US-09-746-783-197  
Sequence 197, Application US/09746783  
Publication No. US2003004935A1  
GENERAL INFORMATION:  
APPLICANT: Jacobs, Kenneth  
McCoy, John M.  
LaValle, Edward R.  
Racie, Lisa A.  
Treacy, Maurica  
Spaulding, Vikki  
Agostino, Michael J.  
Howes, Steven H.  
Fechtel, Kim  
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES  
ENCODING THEM  
NUMBER OF SEQUENCES: 231  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 CambridgePark Drive  
CITY: Cambridge  
STATE: MA  
COUNTRY: U.S.A.  
ZIP: 02140  
COMPUTER READABLE FORM:

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MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/746,783
FILING DATE: 21-Dec-2000
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Milasincic, Debra J.
REGISTRATION NUMBER: 46,931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 197:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: Protein
SEQUENCE DESCRIPTION: SEQ ID NO: 197:
US-09-746-783-197

Query Match 23.8%; Score 163.5; DB 10; Length 167;
Best Local Similarity 31.6%; Pred.No.:1.2e-09;
Matches 37; Conservative 22; Mismatches 45; Indels 13; Gaps 3;

QY 11 TKICVGRDPTNPSBELTHTLTKLNAENNATFYFKIDNVKARQVVVAGKKYFID 70
DB 54 SRVKEPPKTIKTDGVLQAARYSVEKFNCTNDMLFKESRITRALVQIVKGLKYLE 113
QY 71 FVARETCKESNELTESCE---TKKLGSLDCNARVVVVVPEKKIYPTVTVNWE 124
DB 114 VEGRTCKCQVHLRL-DDCDFTNHTLKQTLSCYSEVVVVPV-----LQHF 160

RESULT 11
US-09-969-834-1
Sequence 1, Application US/09969834
Patent No. US20020102711A1
GENERAL INFORMATION:
APPLICANT: Bandman, Olga
Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN CYSTATIN-LIKE
PROTEIN
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/969,834
FILING DATE: 01-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/471,765
FILING DATE: <Unknown>
APPLICATION NUMBER: US/08/791,522
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/471,765
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749

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REFERENCE/DOCKET NUMBER: PP-0193 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 178 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: 30443  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-969-834-1

Query Match 23.78; Score 163; DB 9; Length 178;  
Best Local Similarity 34.04; Pred. No. 1.4e-09;  
Matches 35; Conservative 20; Mismatches 44; Indels 4; Gaps 2;  
QY 11 TKICVGCPRDIPNTPSPELEETLTHITIKLAENNAATFYFKIDNVKARVQVAGKKYFI 70  
DB 54 SRVKGPFKTIKNDPQVQAARVSYVEKFNCTNDMFLEKESRITRALVQIVNGLKYLE 113  
QY 71 FVARETTCSKE---SNEELTESCETKGLQ--SLDCNAEVVVPWE 110  
DB 114 VEIRGTTCKGNHRL-DCDFQTNHTLKQTLSCYSEWVVPW 155

## RESULT 12

US-09-775-932-14  
Sequence 14, Application US/09775932  
Patent No. US20020137671A1  
GENERAL INFORMATION:  
APPLICANT: University of British Columbia  
TITLE OF INVENTION: Production and use of Modified Cystatins  
FILE REFERENCE: 58069  
CURRENT APPLICATION NUMBER: US/09/775,932  
CURRENT FILING DATE: 2001-02-02  
PRIOR APPLICATION NUMBER: CA99/00717  
PRIOR FILING DATE: 1999-08-05  
PRIOR APPLICATION NUMBER: 60/095,503  
PRIOR FILING DATE: 1998-08-05  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 14  
LENGTH: 121  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-775-932-14

Query Match 20.24; Score 138.5; DB 9; Length 121;  
Best Local Similarity 31.54; Pred. No. 4.2e-07;  
Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;  
QY 10 PTKICVGCPRDIPNTPSPELEETLTHITIKLAENNAATFYFKIDNVKARVQVAGKKYFI 69  
DB 2 PQERWVGLRDLSPDPQVQAARVSYVNGSNIYFRDTHIIKAQSOLVAGIKYFL 61  
QY 70 DFVARETTCSKE---SNEELTESCETKGLQ--SLDCNAEVVVPWE 111  
DB 62 TWEMGSTDCRKRTRVTGDHVDLT-TCPLAAGAQOEKLRCDFEVLVVPWQ 108

## RESULT 13

US-09-775-932-12  
Sequence 12, Application US/09775932  
Patent No. US20020137671A1  
GENERAL INFORMATION:  
APPLICANT: University of British Columbia  
TITLE OF INVENTION: Production and use of Modified Cystatins  
FILE REFERENCE: 58069  
CURRENT APPLICATION NUMBER: US/09/775,932  
CURRENT FILING DATE: 2001-02-02

PRIOR APPLICATION NUMBER: CA99/00717  
PRIOR FILING DATE: 1999-08-05  
PRIOR APPLICATION NUMBER: 60/095,503  
PRIOR FILING DATE: 1998-08-05  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: Patent in Ver. 2.0  
SEQ ID NO 12  
LENGTH: 128  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-775-932-12

Query Match 20.24; Score 138.5; DB 9; Length 128;  
Best Local Similarity 31.54; Pred. No. 4.5e-07;  
Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;  
QY 10 PTKICVGCPRDIPNTPSPELEETLTHITIKLAENNAATFYFKIDNVKARVQVAGKKYFI 69  
DB 9 PQERWVGLRDLSPDPQVQAARVSYVNGSNIYFRDTHIIKAQSOLVAGIKYFL 68  
QY 70 DFVARETTCSKE---SNEELTESCETKGLQ--SLDCNAEVVVPWE 111  
DB 69 TWEMGSTDCRKRTRVTGDHVDLT-TCPLAAGAQOEKLRCDFEVLVVPWQ 115

## RESULT 14

US-09-940-497-2  
Sequence 2, Application US/09940497  
Patent No. US20020052476A1  
GENERAL INFORMATION:  
APPLICANT: NI et al.  
TITLE OF INVENTION: Human Cystatin E  
FILE REFERENCE: PF202PID2  
CURRENT APPLICATION NUMBER: US/09/940,497  
CURRENT FILING DATE: 2001-08-29  
PRIOR APPLICATION NUMBER: US 09/241,376  
PRIOR FILING DATE: 1999-02-02  
PRIOR APPLICATION NUMBER: US 08/744,138  
PRIOR FILING DATE: 1996-11-05  
PRIOR APPLICATION NUMBER: US 08/461,030  
PRIOR FILING DATE: 1995-06-05  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: Patent in version 3.1  
SEQ ID NO 2  
LENGTH: 149  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-940-497-2

Query Match 20.24; Score 138.5; DB 9; Length 149;  
Best Local Similarity 31.54; Pred. No. 5.5e-07;  
Matches 34; Conservative 22; Mismatches 45; Indels 7; Gaps 3;  
QY 10 PTKICVGCPRDIPNTPSPELEETLTHITIKLAENNAATFYFKIDNVKARVQVAGKKYFI 69  
DB 30 PQERWVGLRDLSPDPQVQAARVSYVNGSNIYFRDTHIIKAQSOLVAGIKYFL 89  
QY 70 DFVARETTCSKE---SNEELTESCETKGLQ--SLDCNAEVVVPWE 111  
DB 90 TWEMGSTDCRKRTRVTGDHVDLT-TCPLAAGAQOEKLRCDFEVLVVPWQ 136

## RESULT 15

US-08-849-303-16  
Sequence 16, Application US/08849303  
Publication No. US20030221209A1  
GENERAL INFORMATION:  
APPLICANT: Atkinson, Howard J.  
APPLICANT: McPherson, Michael J.  
APPLICANT: Uffwin, Peter E.  
TITLE OF INVENTION: MODIFIED PROTEINASE INHIBITORS  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:



UB-10-661-784-3.rapb

Mon Sep 27 08:32:57 2004

ADDRESSEE: Klauber & Jackson  
STREET: 411 Hackensack Avenue, 4th Floor  
CITY: Hackensack  
STATE: New Jersey  
COUNTRY: USA  
ZIP: 07601  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/849,303  
FILING DATE: 21-MAY-1997  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Jackson Esq., David A.  
REGISTRATION NUMBER: 26,742  
REFERENCE/DOCKET NUMBER: 1321-1-003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-487-5800  
TELEFAX: 201-343-1684  
TELEX: 133521  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 112 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-849-303-16

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Query Match      20.0%; Score 137.5; DB 8; Length 112;
Best Local Similarity 28.8%; Pred. NO. 4.9e-07;
Matches 32; Conservative 25; Mismatches 35; Indels 19; Gaps 4;

24 NSPELSELTHTITKLNAAENNATPEKIDNVKARVQVWAGKYPIDFVARETTSKSN 83
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12 NEEGVOEALSPAVSEFNKRSNDAYQSRVVRVRAARQVWSGMYFLDELGRITCTK--S 69
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84 ELUTEESC-----ETKKLGQSLDCNAEYVVVVPPEKKIYPTVTNHWEEC 126
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

70 QANLDCSPHPNPHLKREKL-----CSQVYVVPWNN-----TINLVAFSQ 111
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Search completed: September 24, 2004, 14:13:04  
Job time : 45.704 secs

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